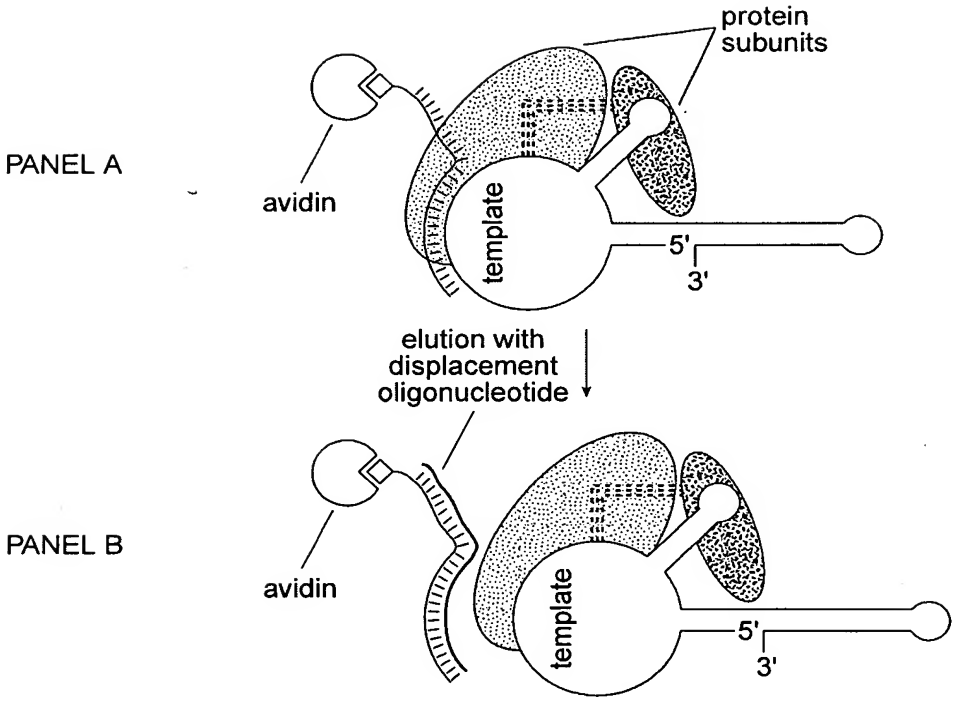


FIG. 1

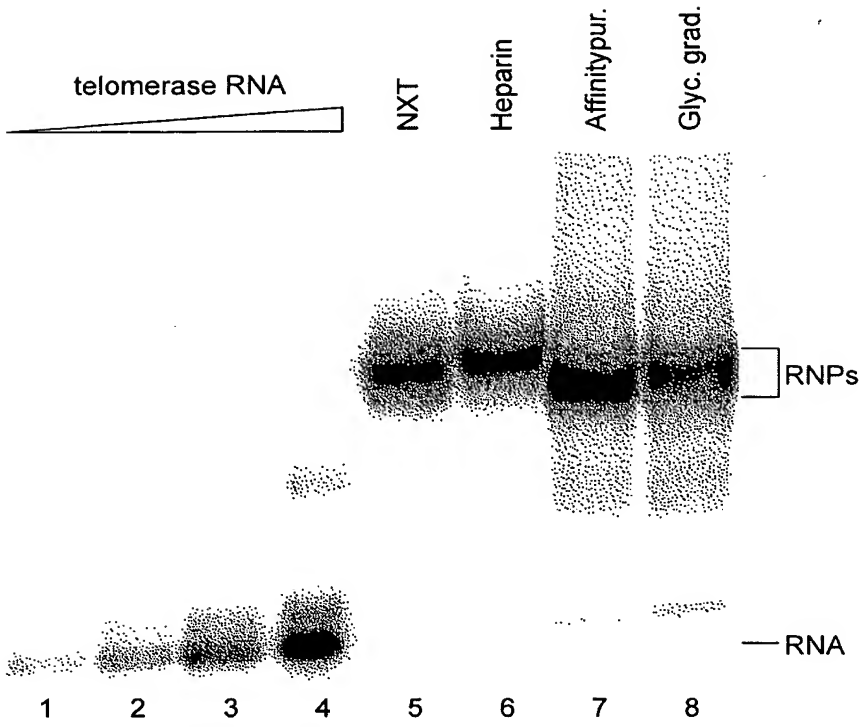

telomerase RNA
NXT
Heparin
Affinitypur.
Glyc. grad.
RNPs
RNA
1 2 3 4 5 6 7 8

FIG. 2

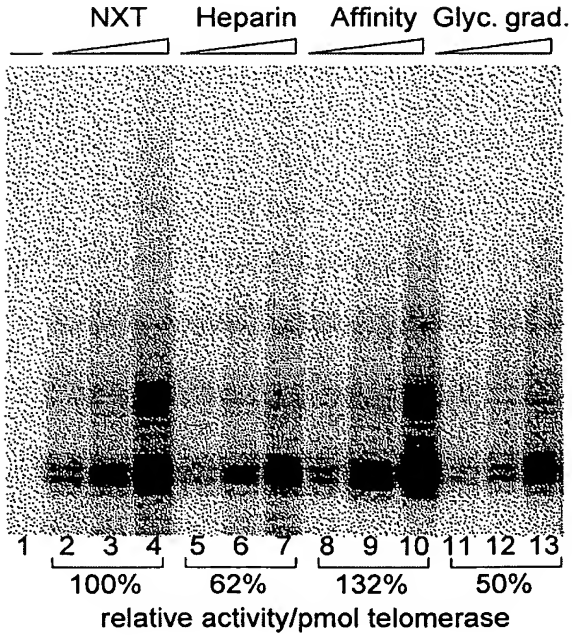

NXT
Heparin
Affinity
Glyc. grad.
1 2 3 4 5 6 7 8 9 10 11 12 13
100%
62%
132%
50%
relative activity/pmol telomerase

FIG. 3

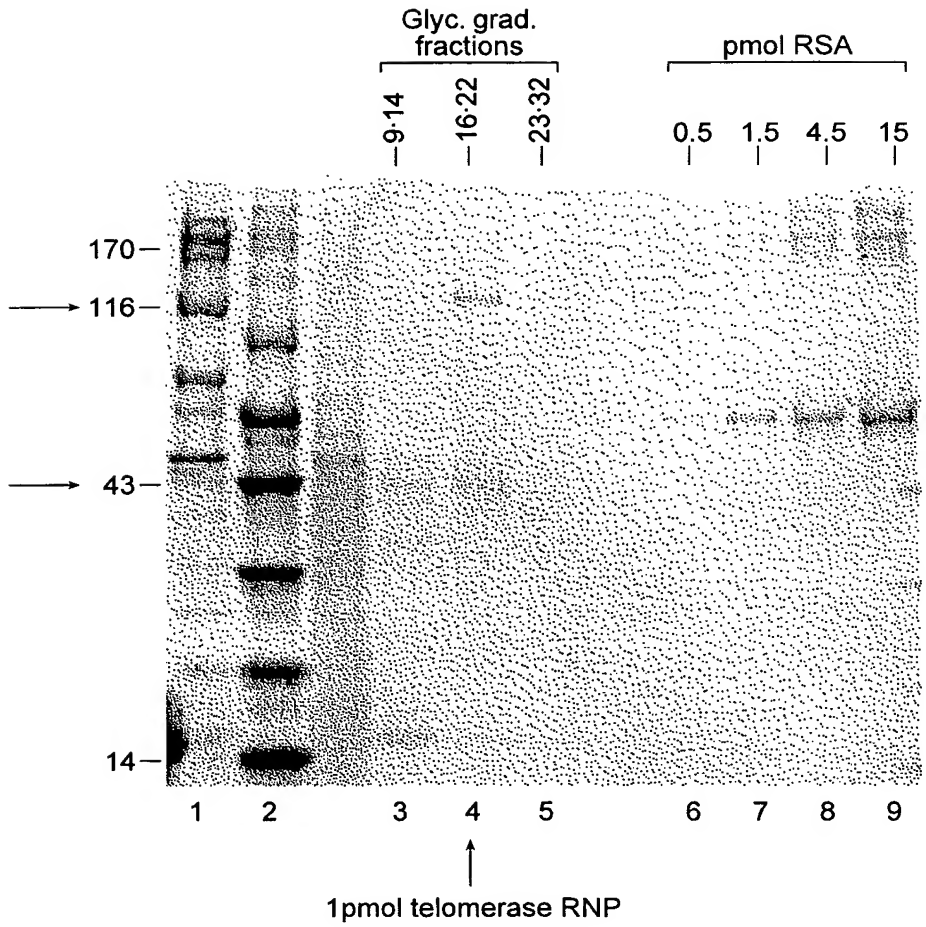

Glyc. grad. fractions
9·14
16·22
23·32
pmol RSA
0.5
1.5
4.5
15
170
116
43
14
1
2
3
4
5
6
7
8
9
1pmol telomerase RNP

FIG. 4

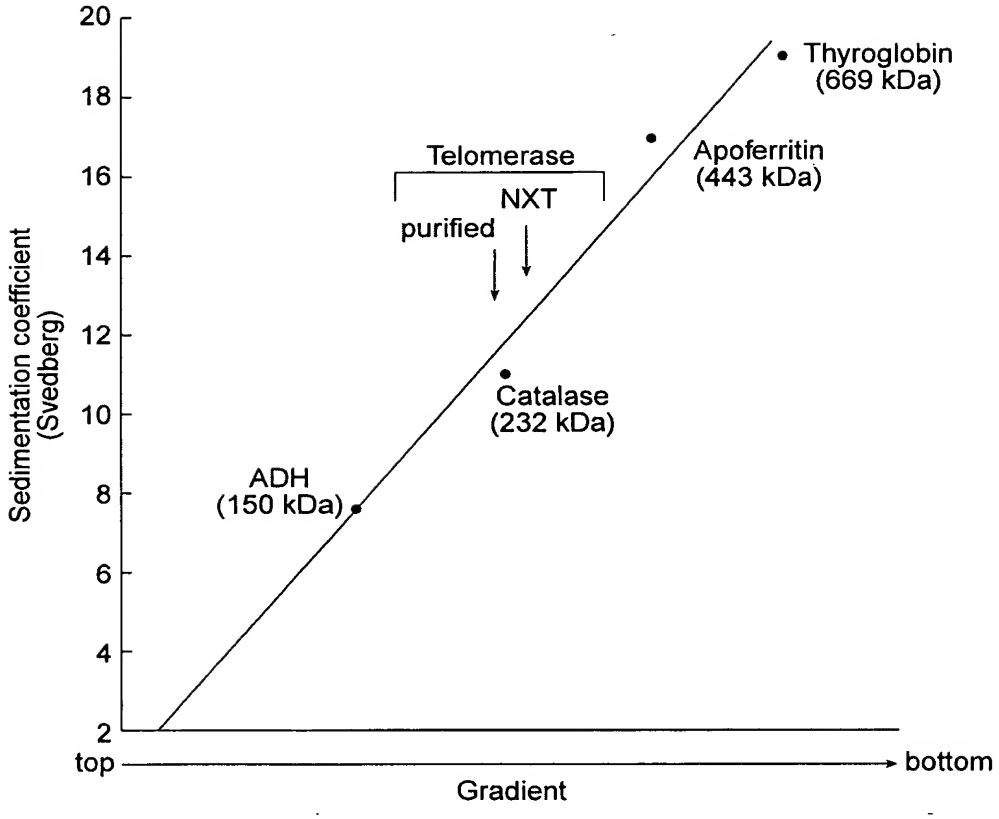

20
18
16
14
12
10
8
6
4
2
Sedimentation coefficient (Svedberg)
Thyroglobin (669 kDa)
Apoferritin (443 kDa)
Telomerase
NXT
purified
Catalase (232 kDa)
ADH (150 kDa)
top
bottom
Gradient

FIG. 5

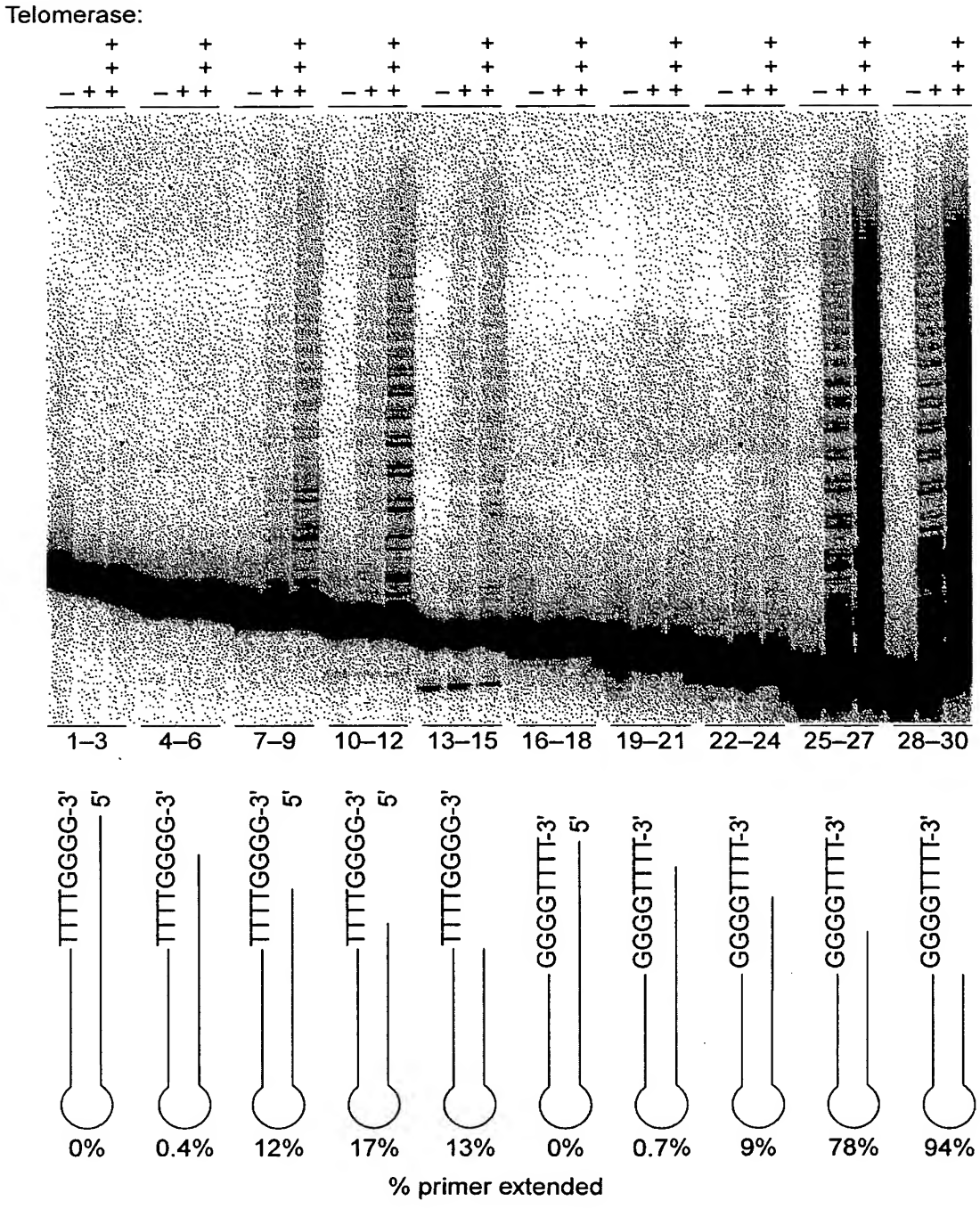

Telomerase:
1–3
4–6
7–9
10–12
13–15
16–18
19–21
22–24
25–27
28–30
TTTTGGGG-3'
5'
GGGGTTTT-3'
0%
0.4%
12%
17%
13%
0%
0.7%
9%
78%
94%
% primer extended

FIG. 6

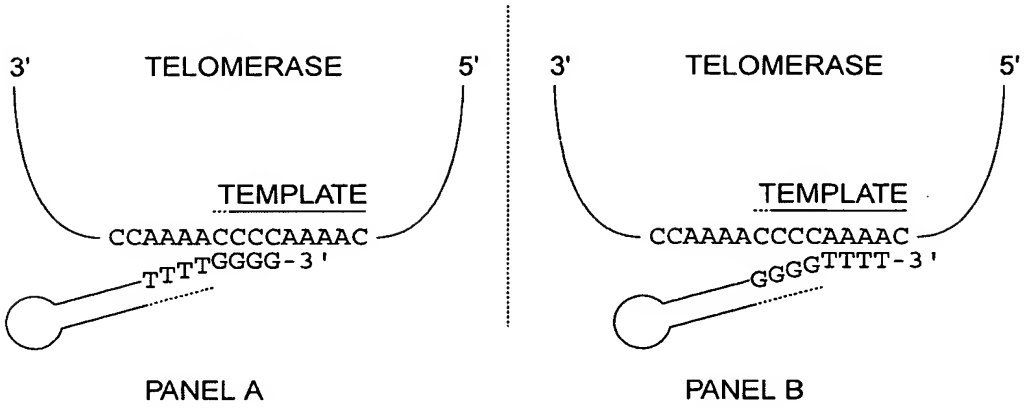


FIG. 7

```
   1  CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG
  51  GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
 101  TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
 151  GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
 201  TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
 251  CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
 301  AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
 351  AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
 401  TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTC
 451  CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
 501  GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
 551  AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG
 601  TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
 651  TTGAGACAAT TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA
 701  AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
 751  CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
 801  TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
 851  TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
 901  TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
 951  AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
1001  TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
1051  AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC
1101  AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATTT
1151  CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
1201  GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
1251  TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
1301  GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351  AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
1401  AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
1451  ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAAA
1501  GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551  CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
1601  ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
1651  AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701  AAGATTTATT TTTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
1751  GGGGTTTTGG GG
```

FIG. 11

FIG. 8

```
   1  AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
  51  AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101  ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151  TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
 201  TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251  TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
 301  AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351  CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT
 401  TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCA
 451  ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
 501  CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551  ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601  GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651  ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701  GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
 751  GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
 801  ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
 851  AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC
 901  AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951  GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001  CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
1051  TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA
1101  TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151  TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
1201  CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251  AAAAGAAAGT TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC
1301  AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351  GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT
1401  ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451  CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501  AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551  TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601  GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651  ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701  TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG
1751  AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801  TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851  AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA
1901  ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC
1951  AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
2001  CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051  TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101  TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
2151  AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201  AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
2251  CCAATATAAT TACATTAACT TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301  GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC ATTTTATTAT
2351  GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
```

FIG. 9A

```
2401  CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451  TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501  ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551  GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601  GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651  TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701  AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751  CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801  CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACTCT
2851  CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901  AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951  TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001  CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051  ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101  AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151  GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201  CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG TCTTATATAC
3251  TGGGGTTTTG GGGTTTTGGG GTTTTGGGG
```

FIG. 9B

```
   1  MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
  51  LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
 101  SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
 151  IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
 201  ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTR IFYCTHFNRN
 251  NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
 301  LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
 351  YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELIH
 401  KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
 451  LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
 501  EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
 551  NSHLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
 601  TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
 651  FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLIVEAKQ
 701  RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
 751  ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
 801  INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
 851  SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
 901  HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
 951  LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
1001  KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A
```

FIG. 10

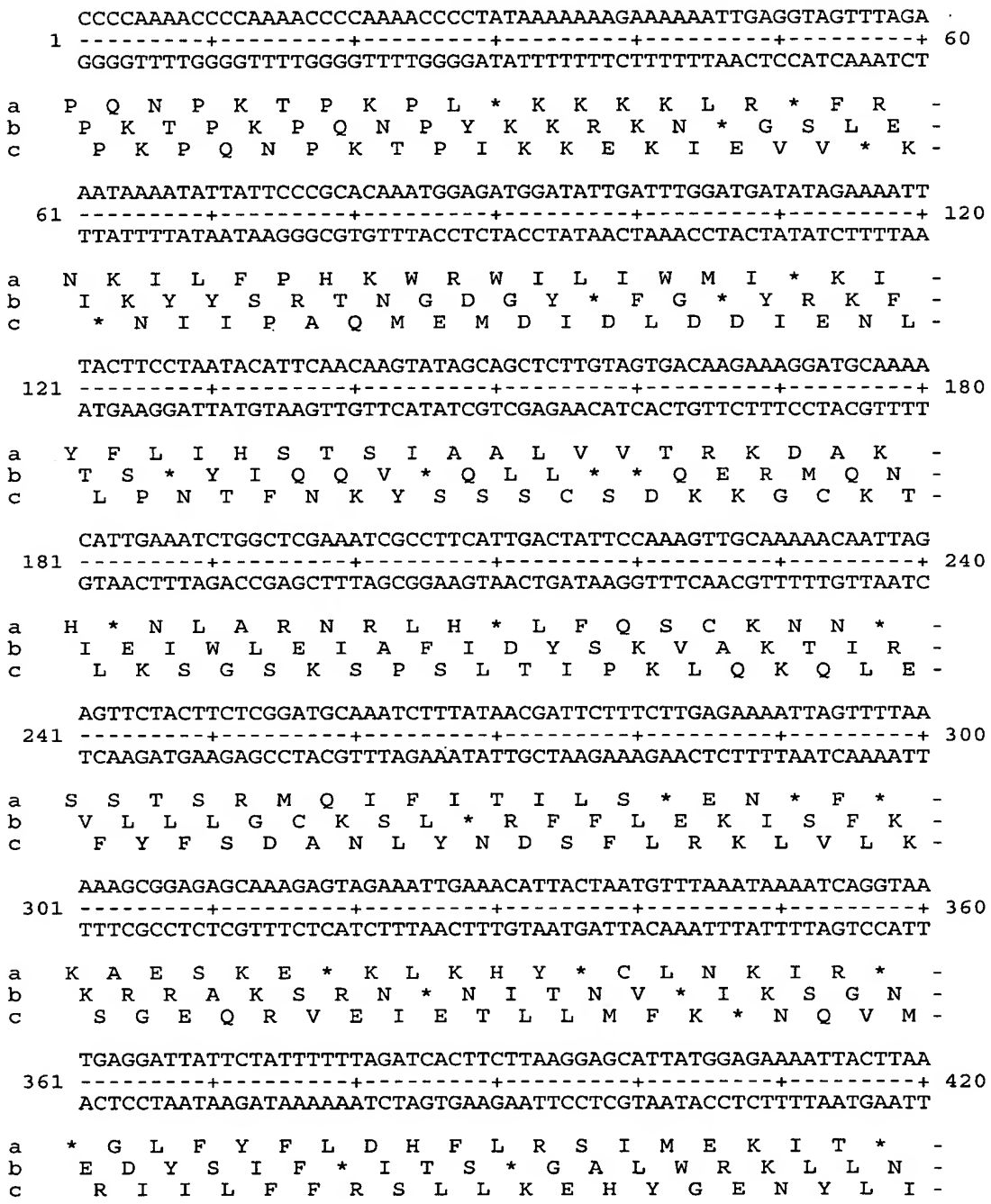

CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAAGAAAAAATTGAGGTAGTTTAGA
1 ---------+---------+---------+---------+---------+---------+ 60
GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTTCTTTTTTAACTCCATCAAATCT
a P Q N P K T P K P L * K K K K L R * F R -
b P K T P K P Q N P Y K K R K N * G S L E -
c P K P Q N P K T P I K K E K I E V V * K -
AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT
61 ---------+---------+---------+---------+---------+---------+ 120
TTATTTTATAATAAGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA
a N K I L F P H K W R W I L I W M I * K I -
b I K Y Y S R T N G D G Y * F G * Y R K F -
c * N I I P A Q M E M D I D L D D I E N L -
TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
121 ---------+---------+---------+---------+---------+---------+ 180
ATGAAGGATTATGTAAGTTGTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT
a Y F L I H S T S I A A L V V T R K D A K -
b T S * Y I Q Q V * Q L L * * Q E R M Q N -
c L P N T F N K Y S S S C S D K K G C K T -
CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
181 ---------+---------+---------+---------+---------+---------+ 240
GTAACTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC
a H * N L A R N R L H * L F Q S C K N N * -
b I E I W L E I A F I D Y S K V A K T I R -
c L K S G S K S P S L T I P K L Q K Q L E -
AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
241 ---------+---------+---------+---------+---------+---------+ 300
TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT
a S S T S R M Q I F I T I L S * E N * F * -
b V L L L G C K S L * R F F L E K I S F K -
c F Y F S D A N L Y N D S F L R K L V L K -
AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
301 ---------+---------+---------+---------+---------+---------+ 360
TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT
a K A E S K E * K L K H Y * C L N K I R * -
b K R R A K S R N * N I T N V * I K S G N -
c S G E Q R V E I E T L L M F K * N Q V M -
TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
361 ---------+---------+---------+---------+---------+---------+ 420
ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT
a * G L F Y F L D H F L R S I M E K I T * -
b E D Y S I F * I T S * G A L W R K L L N -
c R I I L F F R S L L K E H Y G E N Y L I -

FIG. 12A

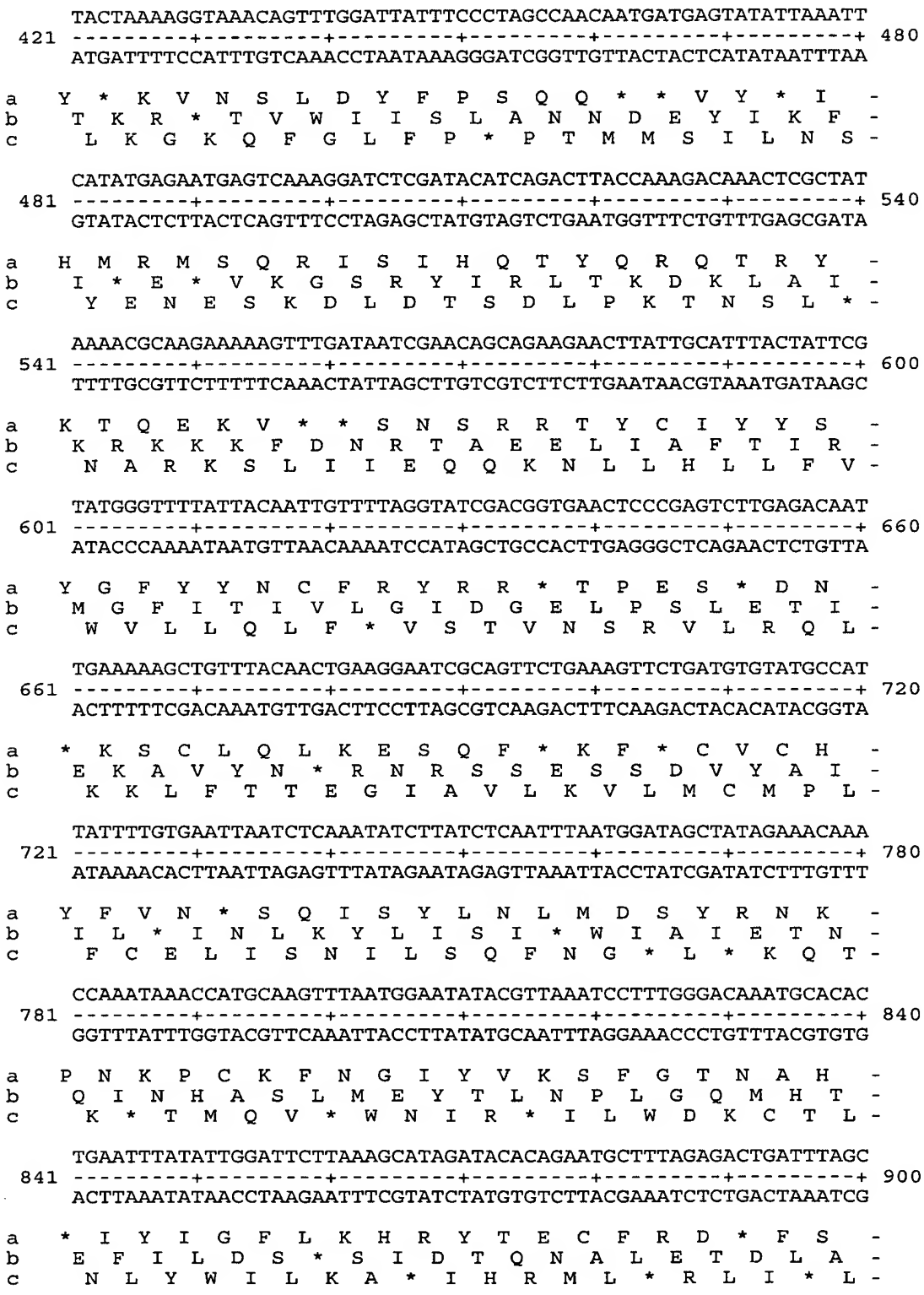

TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
421 480
ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA
a Y * K V N S L D Y F P S Q Q * * V Y * I -
b T K R * T V W I I S L A N N D E Y I K F -
c L K G K Q F G L F P * P T M M S I L N S -
CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
481 540
GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA
a H M R M S Q R I S I H Q T Y Q R Q T R Y -
b I * E * V K G S R Y I R L T K D K L A I -
c Y E N E S K D L D T S D L P K T N S L * -
AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG
541 600
TTTTGCGTTCTTTTTCAAACTATTAGCTTGTCGTCTTCTTGAATAACGTAAATGATAAGC
a K T Q E K V * * S N S R R T Y C I Y Y S -
b K R K K K F D N R T A E E L I A F T I R -
c N A R K S L I I E Q Q K N L L H L L F V -
TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACTCCCGAGTCTTGAGACAAT
601 660
ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA
a Y G F Y Y N C F R Y R R * T P E S * D N -
b M G F I T I V L G I D G E L P S L E T I -
c W V L L Q L F * V S T V N S R V L R Q L -
TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
661 720
ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA
a * K S C L Q L K E S Q F * K F * C V C H -
b E K A V Y N * R N R S S E S S D V Y A I -
c K K L F T T E G I A V L K V L M C M P L -
TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
721 780
ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT
a Y F V N * S Q I S Y L N L M D S Y R N K -
b I L * I N L K Y L I S I * W I A I E T N -
c F C E L I S N I L S Q F N G * L * K Q T -
CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
781 840
GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG
a P N K P C K F N G I Y V K S F G T N A H -
b Q I N H A S L M E Y T L N P L G Q M H T -
c K * T M Q V * W N I R * I L W D K C T L -
TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
841 900
ACTTAAATATAACCTAAGAATTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG
a * I Y I G F L K H R Y T E C F R D * F S -
b E F I L D S * S I D T Q N A L E T D L A -
c N L Y W I L K A * I H R M L * R L I * L -

FIG. 12B

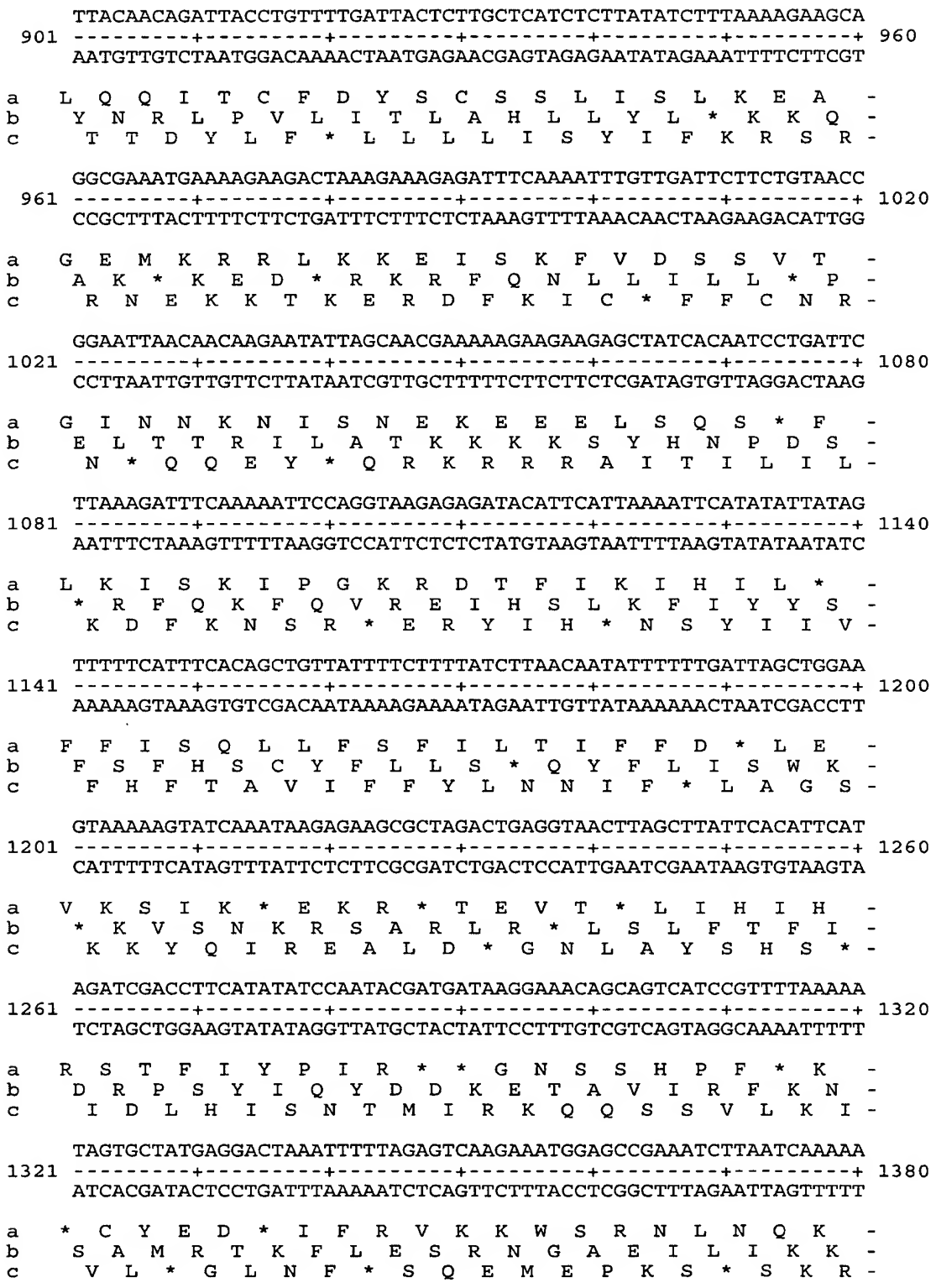

TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
901 960
AATGTTGTCTAATGGACAAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT
a L Q Q I T C F D Y S C S S L I S L K E A -
b Y N R L P V L I T L A H L L Y L * K K Q -
c T T D Y L F * L L L L I S Y I F K R S R -
GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC
961 1020
CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG
a G E M K R R L K K E I S K F V D S S V T -
b A K * K E D * R K R F Q N L L I L L * P -
c R N E K K T K E R D F K I C * F F C N R -
GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAAGAGCTATCACAATCCTGATTC
1021 1080
CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTTCTCGATAGTGTTAGGACTAAG
a G I N N K N I S N E K E E E L S Q S * F -
b E L T T R I L A T K K K K S Y H N P D S -
c N * Q Q E Y * Q R K R R R A I T I L I L -
TTAAAGATTTCAAAAATTCCAGGTAAGAGAGATACATTCATTAAAATTCATATATTATAG
1081 1140
AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC
a L K I S K I P G K R D T F I K I H I L * -
b * R F Q K F Q V R E I H S L K F I Y Y S -
c K D F K N S R * E R Y I H * N S Y I I V -
TTTTTCATTTCACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTTGATTAGCTGGAA
1141 1200
AAAAAGTAAAGTGTCGACAATAAAAGAAAATAGAATTGTTATAAAAAACTAATCGACCTT
a F F I S Q L L F S F I L T I F F D * L E -
b F S F H S C Y F L L S * Q Y F L I S W K -
c F H F T A V I F F Y L N N I F * L A G S -
GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACTTAGCTTATTCACATTCAT
1201 1260
CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA
a V K S I K * E K R * T E V T * L I H I H -
b * K V S N K R S A R L R * L S L F T F I -
c K K Y Q I R E A L D * G N L A Y S H S * -
AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
1261 1320
TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTTT
a R S T F I Y P I R * * G N S S H P F * K -
b D R P S Y I Q Y D D K E T A V I R F K N -
c I D L H I S N T M I R K Q Q S S V L K I -
TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
1321 1380
ATCACGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT
a * C Y E D * I F R V K K W S R N L N Q K -
b S A M R T K F L E S R N G A E I L I K K -
c V L * G L N F * S Q E M E P K S * S K R -

FIG. 12C

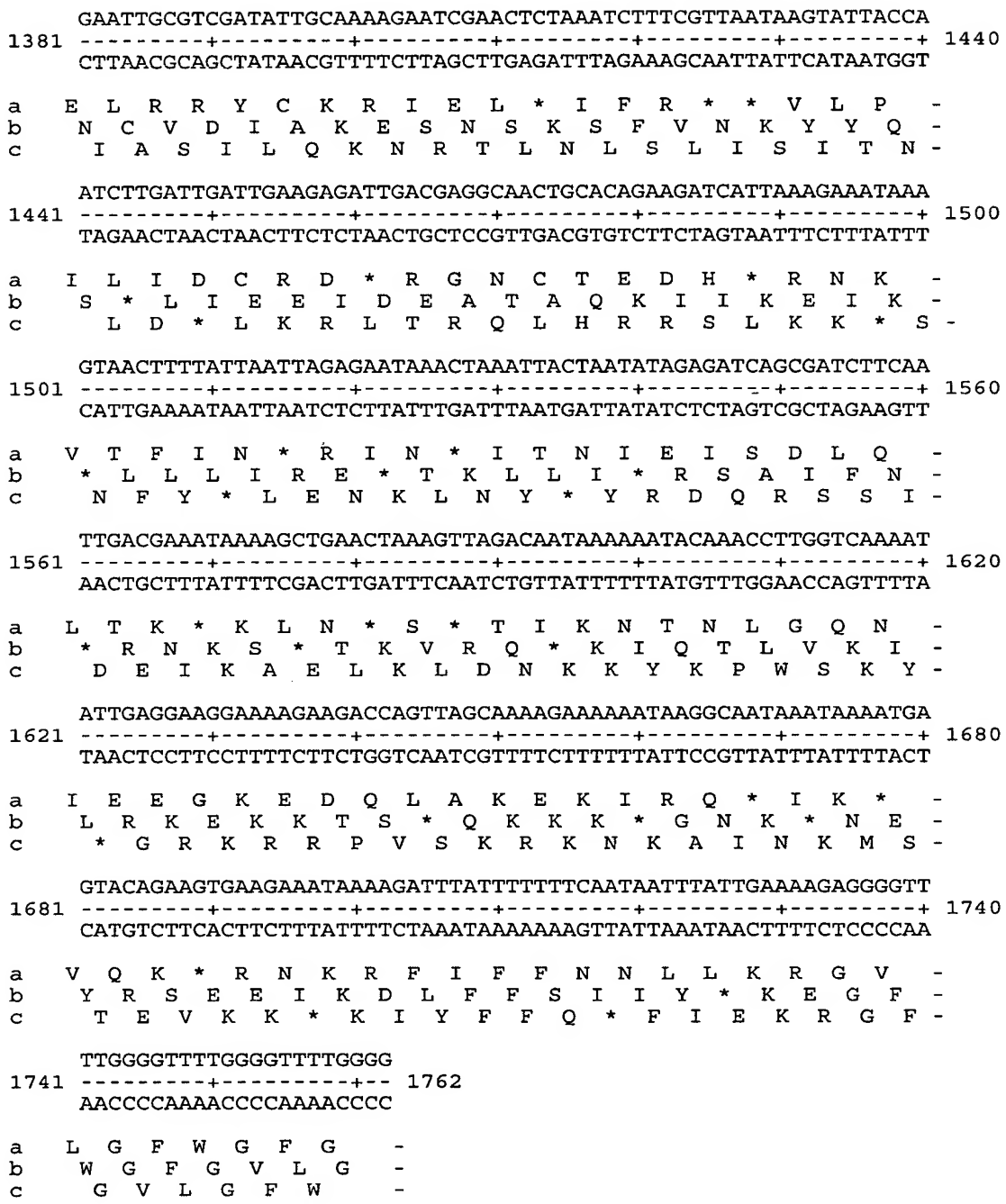

GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA
1381 ---------+---------+---------+---------+---------+---------+ 1440
CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT
a E L R R Y C K R I E L * I F R * * V L P -
b N C V D I A K E S N S K S F V N K Y Y Q -
c I A S I L Q K N R T L N L S L I S I T N -
ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
1441 ---------+---------+---------+---------+---------+---------+ 1500
TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT
a I L I D C R D * R G N C T E D H * R N K -
b S * L I E E I D E A T A Q K I I K E I K -
c L D * L K R L T R Q L H R R S L K K * S -
GTAACTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
1501 ---------+---------+---------+---------+---------+---------+ 1560
CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT
a V T F I N * R I N * I T N I E I S D L Q -
b * L L L I R E * T K L L I * R S A I F N -
c N F Y * L E N K L N Y * Y R D Q R S S I -
TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
AACTGCTTTATTTTCGACTTGATTTCAATCTGTTATTTTTTATGTTTGGAACCAGTTTTA
a L T K * K L N * S * T I K N T N L G Q N -
b * R N K S * T K V R Q * K I Q T L V K I -
c D E I K A E L K L D N K K Y K P W S K Y -
ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAAATAAGGCAATAAATAAAATGA
1621 ---------+---------+---------+---------+---------+---------+ 1680
TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTTTATTCCGTTATTTATTTTACT
a I E E G K E D Q L A K E K I R Q * I K * -
b L R K E K K T S * Q K K K * G N K * N E -
c * G R K R R P V S K R K N K A I N K M S -
GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT
1681 ---------+---------+---------+---------+---------+---------+ 1740
CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAAATAACTTTTCTCCCCAA
a V Q K * R N K R F I F F N N L L K R G V -
b Y R S E E I K D L F F S I I Y * K E G F -
c T E V K K * K I Y F F Q * F I E K R G F -
TTGGGGTTTTGGGGTTTTGGGG
1741 ---------+---------+-- 1762
AACCCCAAAACCCCAAAACCCC
a L G F W G F G -
b W G F G V L G -
c G V L G F W -

FIG. 12D


2 EVDVQNQADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL 51
19 ELELEMQENQNDIQVRVK....IDDPKQY..LVNVTAACLLQEGSYYQDK 62
52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL 100
63 DERRYIITKALL....EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF. 107
101 SSSDVSDRQKLQCFGFQLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM 150
108 .....CVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144
151 IGNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGA 200
145 FDATEFKNLY.....LDRILSQDIRKELTFRKCLQRCVRSKF 181
201 ADMNE...PRCCSTCKYNVKNEKDHFLNNINVPNWNNMKSRTRIFYCTHF 247
182 SEFNEYQLGKYCTES..QRKKTMFRYLSVTNKQKWDQTKKK..... 220
248 NRNNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDKVIEKI 297
221 .RKENLLTKLQAIKESEDKSKRETG.....DIMNVEDAIKALKPAVMKKI 264
298 AYMLEKVKDFNFNYYLTKSCPLPENWRERKQKIENLINKTREEKSKYYEE 347
265 AKRQNAMK..... .....KHMKAPKIPNSTLESKYLTFKD 294
348 LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKHE 397
295 LIKFCHISEP.....KERVYKILGKKYPKTEEEYKAAFGDSASAPFN.PE 338
398 LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL 447
339 LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSN.. 386
448 VVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE 497
387 .....ILKAGVSD..... 394
498 KEVEEWKKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTTNT 547
395 .....TTHS 398
548 KLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL 597
399 IVINK.....ICEPKAVENSKM 415
598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVID 647
416 F..PLQFFSAIEAVN.EAVTKGFKAKK...RENMNLKGQIEAVKE..VVE 457
648 SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVE 697
458 KTDEEKKDM.....ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496
698 AKQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS 747
497 IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGL 546
748 FYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFI 797
547 MVKQRCEKSSFYIFSSPSSQCNKCYLEVDL..... 576

FIG. 13A

```
798  EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
577  .......PGDELRPSMQKLLQEKGKLGGG..TDFPYECIDEWTKNKTHVD 617

847  WIGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKKLKSFLM 896
618  NIVILSDMMIAEGYSDINVRGSSIVNSI.............KKYKDEVN 653

897  NNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEYKD.HFKKNLAM 945
654  PNIKIF...AVDLEGYG.............KCLNLGDEFNENNYIKIFGM 687

946  SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE 995
688  SDSI...............LKFISAKQGGA...............NMVE 706

996  IFSTKKYIFNRVC 1008
707  VI..KNFALQKIG 717
```

FIG. 13B

```
132  LSTQKQYFFQDEWNQVRAMIGNEL.FRHLYTKYLIFQRTSE..GTLVQFC 178
  1  MSRRNQ.......KKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQI  43

179  GNNVFDHLKVNDKFDKKQKGGAADMNEPRCCSTCKYNVKNEKDHFLNNIN 228
 44  KEEDLKLLKFKNQDQDGNSGNDDDDEE.........NNSNKQQELLRRVN  84

229  VPNWNNMKSRTRIFYCTHFNRNNQFFKKHEFVSNKNNISAMDRAQTIFTN 278
 85  .................QIKQQVQLIKK...VGSKVEKDLNLNEDENKKN 114

279  IFRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRERKQ 328
115  GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY 164

329  KIENLINKTREEKSKYYEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
165  DTEKWFEISHDQK..............NYVSIYANQKTSYCWWLKDYFNK 200

378  RNRKNFQKKVKKYVELNKHELIHKNLLLEKINTREISWMQVETSAKHFYY 427
201  NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID......  242

428  FDHENIYVLWKLLRWI..FEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNI 475
243  VNFDNNLCILALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290

476  WDVIMKMSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP 525
291  FAVVFSHR..........HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ  330

526  IMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNY 575
331  VYSFSTDLKLVD..TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL  378
```

FIG. 14A

```
576  DDVMKKYEEFVCKWKQVGQPKLF. . ....FATMDIEKCYDS..VNREK  615
379  NVLLKKVKH  ANLNLVSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQK  426

516  LSTFL......KTTKLLSSDFWIMTAQILKRKNNI..VIDSKNFRKKEMK  657
427  LENLLLSIKQSKNLKFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQ  476

558  DYFRQKFQKIALEGGQYPTLFSVLEN..EQNDLNAKKTLIVEAKQRNYFK  705
477  EETPETKDETPSESTSGMKFFDHLSELTELEDFSVN....LQATQEIY..  520

706  KDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEE  755
521  .DSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNI.....YETLNN  564

756  SSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFIEKLINVSR  305
565  .....LKRCSVNISNPHGNISYELTN.........KDSTFYKFKLTLNQE  500

806  ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK  855
601  LQHAKYTFK..QNEFQFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ  648

856  TLALMPNINLRIEGILCTLNLNMQT..KKASMWLKK..KLKSFLMNNITH  901
649  NVNI.......IASLLYPNNIQKNPFNKPNLLFFKQFEQLKNLENVSINC  691

902  YFRKTI...TTEDFANKTLNKLFISGGYKYMQCAKEYKDHFKKNLAMSSM  948
692  ILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPEL  741

949  IDLEVSKIIYSVT.............RAFFKYLVCNIKDT..IFGEEHY  982
742  NQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDF  791

983  PDFFLS  TLKHFIEIFSTKKY IFNRVCMILKAKEAKLKSDQCQSLIQ  1028
792  DQNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLK   840
```

FIG. 14B

```
  4  DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK......   47
617  NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP  666

 48  .......LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVE....IETLLM   86
667  FNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL  716
```

FIG. 15

```
  1  MEMDIDLDDIENL.....LPNTFNKYSSSCSDKKGCKTLKSGSKSPS...   42
491  IELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLEC  540

 43  .LTIPKLQKQ......LEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL   85
541  ALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL  589
```

FIG. 16

```
telomerase p43   LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La         ICHQUEYYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA      ICEQIEYYFGDHNLPRDKFLKQQI.LLDDGWVPLETMIK
Drosophila La    ILRQVEYYFGDANLNRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhp1p      CLKQVEFYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT
```

FIG. 18

```
   1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
  61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc
 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt cttgaggtgg ctgagtctga tcctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
 421 ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa
 481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
 541 caaaaatttg tatcttgata ggatactttc ataagatatt cgtaaggaac tcactttccg
 601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tcctaactct accttggaat caaagtactt
 961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
1021 gatccttggt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
1081 tgcatctgca cccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaat
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
1261 cggtgtttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga
1441 agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc
1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac
1621 tgcaatcttc tctgatgttt ctggttctat gagtacctca atgtcaggtg gagccaagaa
1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
1801 ttacttagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aacttttgca
1861 agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac
1921 aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
2041 tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgcct
2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
2161 aatcttaaag ttcatttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
2281 ctcaccccac ttttttgttt tattgcatag ccattatgaa atttaaatta ttatctattt
2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
2401 aaagaacaaa aaagattaaa a
```

FIG. 19

```
                                  Motif A                                   Motif B

Consensus                   h--hDh---h--h                          h---+-QG---SP
telomerase p123     GQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL-100-KFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFL
Dong (LINE)         KNRNLHCTYDDYKKAFDSIPHSWLIQVLEIYKIN- 28-RQIAIKKGIYQGDSLSPLWFCLALNPLSHQLHNDR
al S.c. (groupII)   FGGSNWFREVDLKKCFDTISHDLIIKELKRYISD- 26-HVPVGPRVCVQGAPTSPALCNAVLLRLDRRLAGLA
HIV-RT              LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-  7-GIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRKQN
L8543.12            VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN- 68-KCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFK

                             Motif C                            Motif D          Motif E

Consensus                  h--YhDDhhh                          Gh-h---K         h-hLGh-h
telomerase p123     -14-LMRLTDDYLLITTQENN-0-AVLFIEKLINVSRENGFKFNMKKLQT-23-QDYCDWIGISI
Dong (LINE)         -16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLDKCKT-25-KCLYKYLGFQQ
al S.c. (groupII)   -55-YVRYADDILIGVLGSKN-2-KIIKRDLNNFLNS.LGLTINEEKTLI- 4-ETPARFLGYNI
HIV-RT              - 4-IYQYMDDLYVGSHLEIG-1-HRTKIEELRQHLLRWGLTTPDKKHQK- 0-EPPFLWMGYEL
L8543.12            - 8-ILKLADDFLIISTDQQQ........VINIKKLAMGGFQKYNAKANR-41-IRSKSSKGIFR
```

FIG. 17

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLA
VYIRNELYIRTTTNYIVAFCVVHKNTQPFIEKYFNKAVLLPNDL
LEVCEFAQVLYIFDATEFKNLYLDRILSQDIRKELTFRKCLQRC
VRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTKKK
RKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKI
AKRQNAMKKHMKAPKIPNSTLESKYLTFKDLIKFCHISEPKERV
YKILGKKYPKTEEEYKAAFGDSASAPFNPELAGKRMKIEISKTW
ENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGVSDTT
HSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKR
ENMNLKGQIEAVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIG
KQYINSIELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGA
KKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL
EVDLPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHV
DNIVILSDMMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFA
VDLEGYGKCLNLGDEFNENNYIKIFGMSDSILKFISAKQGGANM
VEVIKNFALQKIGQK

FIG. 20

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQIK
EEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVNQIKQ
QVQLIKKVGSKVEKDLNLNEDENKKNGLSEQQVKEEQLRTITEE
QVKYQNLVFNMDYQLDLNESGGHRRHRRETDYDTEKWFEISHDQ
KNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVSINRLETEAEFY
AFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERF
NILNIRSSYTRNQYNFEKIGELLETIFAVVFSHRHLQGIHLQVP
CEAFQYLVNSSSQISVKDSQLQVYSFSTDLKLVDTNKVQDYFKF
LQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNLVSIP
TQFNFDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNL
KFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQEETPETKD
ETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIYDSLHKLLI
RSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLKRCSVNI
SNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFN
NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPN
NIQKNPFNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEF
LEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPELNQVYINQ
QLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFD
QNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQ
ELLKACDEKGVLVKAYYKFPLCLPTGTYYDYNSDRW

FIG. 22

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKI
ARNEDVNNSLFCHSANVNVTLLKGAAWKMFHSLVGTYAFVDLLI
NYTVIQFNGQFFTQIVGNRCNEPHLPPKWVQRSSSSSATAAQIK
QLTEPVTNKQFLHKLNINSSSFFPYSKILPSSSSIKKLTDLREA
IFPTNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPL
EGTVLDLSHLSRQSPKERVLKFIIVILQKLLPQEMFGSKKNKGK
IIKNLNLLLSLPLNGYLPFDSLLKKLRLKDFRWLFISDIWFTKH
NFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTIVYFR
HDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRI
IPKKSNNEFRIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEY
LRNKRPTSFTKIYSPTQIADRIKEFKQRLLKKFNNVLPELYFMK
FDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFNTNTGVL
KLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTA
LWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS
QDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDK
ILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMNNFHIRSKS
SKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISE
CYKSAFKDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIE
YEVRFTILNGFLESLSSNTSKFKDNIILLRKEIQHLQAYIYIYI
HIVN

FIG. 23

```
   1 tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa
  61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttgattttg tattacaaaa
 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta
 301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa
 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta
 481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa
 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca
 661 tcttaatgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
 721 ttcacaaaca atcaaactta ctaataattc ttactagact gttaacatag acgttaattt
 781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa
 841 tattttgaat ataagatctt cttatacaag aaattaatat aattttgaga aaattggtga
 901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt
 961 acaagttcct tgcgaagcgt tctaatattt agttaactcc tcatcataaa ttagcgttaa
1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaacaa
1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta
1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt
1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
1321 aaagcttgaa aatctacttt tgagtataaa ataatcaaaa aatcttaaat ttttaagatt
1381 aaacttttac acctacgttg cttaagaaac ctccagaaaa cagatattaa aacaagctac
1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga
1501 aactccaagc gaaagcacaa gtggtatgaa atttttgat catctttctg aattaaccga
1561 gcttgaagat ttcagcgtta acttgtaagc tacccaagaa atttatgata gcttgcacaa
1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga
1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
1741 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttcttatg aactgacaaa
1801 taaagattct acttttttata aatttaagct gaccttaaac taagaattat aacacgctaa
1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgcaa aaattgaatc
1921 ttcctcatta gaaagcttag aagatattga tagtctttgc aaatctattg cttcttgtaa
1981 aaatttacaa aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa
2041 tcctttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttgga
2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
2161 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta
2221 tcttgattat actaaattat ttaaaacact tcaatagtta cctgaattaa attaagttta
2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac
2401 cctttagcta atagattttg accaaaacac tgtaagtgat gactctatta aaaagatttt
2461 agaatctata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
2581 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta
2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaaataaa tattaaatat
2701 tgaatatttc tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga
2761 atatatttta gttatttaat tcattatttt aagtaaataa ttatttttca atcatttttt
2821 aaaaaatcg
```

FIG. 21

Oxytricha	LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Euplotes	LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIG. 24

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTTCGCACTACCAAATTCAAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
TCTTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT
GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC
TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAAGCTATTTTTCCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
GAATAGTATTTGCCCACCATTGGAAGGGACCGTATTGGACTTGTCGCATTTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT
AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTTGAAAAAGTTAAGATTAAA
GGATTTTCGGTGGTTGTTCATTTCTGATATTTGGTTCACCAAGCACAATTTTGAAAACTT
GAATCAATTGGCGATTTGTTTCATTTCCTGGCTATTTAGACAACTAATTCCCAAAATTAT
ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
AATGAGGATTATACCAAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG
AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
TAATAATGTCTTACCAGAGCTTTATTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTCAGGGCTCTAGTTTATC
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC
CAGTCCTAGCCAGGACACATTAATTTTAAAACTGGCTGACGATTTCCTTATAATATCAAC
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG
CACAATGAATAATTTCCATATCCGTTCGAAATCTAGTAAAGGGATATTTCGAAGTTTAAT
AGCGCTGTTTAACACTAGAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCATTCGTTCTTACAACG
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAAGCCTATCTTCAAACACATCAAA
ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

FIG. 26

```
                                                                Motif 0
human                                          AKFLHWLMSVYVVELLRSFFYVTETTFQKNR
tez1        ISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNR
EST2        LKDFRWLFISD---IWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVT-
p123        TREISWMQVET-SAKHFYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
                                         . *.    .  ....*** **

                                                                  Motif 1
human       LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL
tez1        TVYFRKDIWKLLCRPFI-TSMKMEAFEKINENNVRMDTQK-TTLPPAVIRLLPKK--NTF
EST2        IVYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLS--NFNHSKMRIIPKKSNNEF
p123        TYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLIPKK--TTF
              ..*.  *  .    *    *                          .* .**

            Motif 2
human       RPIVNMDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
tez1        RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYMKLLTF
EST2        RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123        RPIMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKN-RMFKDPFGFAVFNYDDVMKKY
            * *               *                 *                    . .

                              Motif 3 (A)
tez1        KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS
EST2        KQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
p123        EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN
               . *         .*   *   *** . .      .*   *
```

FIG. 25

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREK
RAERLTSRVKALFSVLNYERA

FIG. 27

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAG
AGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGC
CAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGC
TGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGA
GAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCT
CAACTACGAGCGGGCGCG

FIG. 28

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLVSTF
PNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRKR
TIETSITQNKSARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG
LINAFQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWL
VLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCR
PFITSMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTN
QTLRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLM
FRIVKKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCN
IYRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFLHRRIAD

FIG. 29

ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga
actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta
ccaagtataaggacaaaaagaacaacttccttcccctaaagacttttactttattaatttacttttcaaatatatttcg
ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat
agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc
ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag
gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttgatgcttgcacacgtctagcatg
attgagatattcaaaaatttctatccactacaactcctttaacgcggttttatttttctatttctattctcatgttgtt
ccaaatatgtatcatctcgtattaggctttttccgttttactcctggaatcgtacctttttcactattccccctaatga
ataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa
gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc
actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgcAT
GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTACCTTAAATGATT
ATGTACAACTTGTTTTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAACGCTTGAGAAGCGATGTACAAACG
TCCTTTTCTATTTTTCTTCATTCGACTGTAGTCGGCTTCGACAGTAAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAA
ATGCTCACAGTCAGAGgtatatatatttttgttttgatttttttctattcgggatagctaatatatgggcagCTAATAGC
GAATGTTGTAAAACAGATGTTCGATGAAAGTTTTGAGCGTCGAAGGAATCTACTGATGAAAGGGTTTTCCATGgtaaggt
attctaattgtgaaatatttacctgcaattactgtttcaaagagattgtatttaaccgataaagAATCATGAAGATTTTC
GAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCCTAATTACCTTATATCTATACTTGAGTCAAAA
AATTGGCAACTTTTGTTAGAAATgtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatagTATCGG
CAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTTGAGGCTCTTCCAAATGACAATTACCTTCAGATTTCTG
GCATACCACTTTTTAAAAATAATGTGTTTGAGGAAACTGTGTCAAAAAAAAGAAAGCGAACCATTGAAACATCCATTACT
CAAAATAAAAGCGCCCGCAAAGAAGTTTCCTGGAATAGCATTTCAATTAGTAGGTTTAGCATTTTTTACAGGTCATCCTA
TAAGAAGTTTAAGCAAGgtaactaatactgttatccttcataactaattttagATCTATATTTTAACTTACACTCTATTT
GTGATCGGAACACAGTACACATGTGGCTTCAATGGATTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAG
CAATTGCACAAAGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCTCCTAAAGGTATACCCTTTAATTGA
ACAAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGACACCCACGATG
ATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATCCATTCTTGTTCGAGTGTTTCCT
AAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAAAGgtattgtataaaatttattaccactaacgatttt
accagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTACATTATTTAATGAGTAACATAAAGgtaa
tatgccaaatttttttaccattaattaacaatcagATTTCAGAAATTGAATGGCTAGTCCTTGGAAAAAGGTCAAATGCG
AAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAATATTTGCGGAATTCATCTACTGGCTATACAATTCGTTTATAAT
ACCTATTTTACAATCTTTTTTTTATATCACTGAATCAAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTT
GGAAACTCTTGTGCCGACCCTTTATTACATCAATGAAAATGGAAGCGTTTGAAAAAATAAACGAGgtattttaaagtatt
ttttgcaaaaagctaatattttcagAACAATGTTAGGATGGATACTCAGAAAACTACTTTGCCTCCAGCAGTTATTCGTC
TATTACCTAAGAAGAATACCTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAGgtattaatttttggtcat
caatgtactttacttctaatctattattagcagATGGGTTCAAACAAAAAAATGTTAGTCAGTACGAACCAAACTTTACG
ACCTGTGGCATCGATACTGAAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGC

FIG. 30A

TTCTTACTTTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGGgtaattatataatgcgcgattcctcattattaatttt
gcagGCGTAAGAAGTATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATT
GTTAAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCGAGCTACAAA
AAACTTTGTTAGTGAGGCGTTTTCCTATTgtaagtttatttttttcattggaatttttttaacaaattctttttttagTTGAT
ATGGTGCCTTTTGAAAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTTGATTTTGTGGATTATTG
GACCAAAAGTTCTTCTGAAATTTTTAAAATGCTCAAGGAACATCTCTCTGGACACATTGTTAAGgtataccaattgttga
attgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTCAGGGCTCAATTCTGT
CATCTTTTTTGTGTCATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTTTACGAAAAAGAAAGGATCAGTGTTG
TTACGAGTAGTCGACGATTTCCTCTTTATAACAGTTAATAAAAAGGATGCAAAAAAATTTTTGAATTTATCTTTAAGAGg
tgagttgctgtcattcctaagttctaaccgttgaagGATTTGAGAAACACAATTTTTCTACGAGCCTGGAGAAAACAGTA
ATAAACTTTGAAAATAGTAATGGGATAATAAACAATACTTTTTTTAATGAAAGCAAGAAAAGAATGCCATTCTTCGGTTT
CTCTGTGAACATGAGGTCTCTTGATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAG
AGCTGACGAAACATATGGGGAAATCTTTTTTTTACAAAATTCTAAGgtatactgtgtaactgaataatagctgacaaata
atcagATCGAGCCTTGCATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCAATTCTTGCTGCAATAT
ATATAGGCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTCCCCAAAGAA
TGTTCATAACGGgtgagtacttattttaactagaaaagtcattaattaaccttagATCTTTTGAATGTTATTGGAAGAAA
AATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCCTCTGCAGAAGTCAAATGgtacgtgt
cggtctcgagacttcagcaatattgacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAACCCTCTTTCAAA
TATCATCCATGCTTCGAACAGCTAATATACCAATTTCAGTCATTGACTGATCTTATCAAGCCGCTAAGACCAGTTTTGCG
ACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAtgtcattttcaatttattatatacatcctttattactggtgtc
ttaaacaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctc
gttattagttttgattgacttgtctttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatg
cccattaaacgggagtggttaaacattaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttt
tctataatgaataatgcccgcactaatgcaaaaagacgaagattatcttctaaacaaggggattaagcatatccgaagg
aaaagagagtaatatacccagtgttgttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaatt
ttggtgaccgaattttggtaaaagccccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggat
agtttgaatactaatagctcatttaatgtcttatataaggttttgtttttttcctgacttcaattttgcatgggtgaaaag
aaatagtgttaagccattattggattccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattg
aagcttatgaggcttcaaaaactcctcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagct
gctgaggagaagcctaatttttttgcaaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtat
ctccagcggatccttgatgtcaataacttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctcta
cgcagttaagtgaccaaaggtacc

FIG. 30B

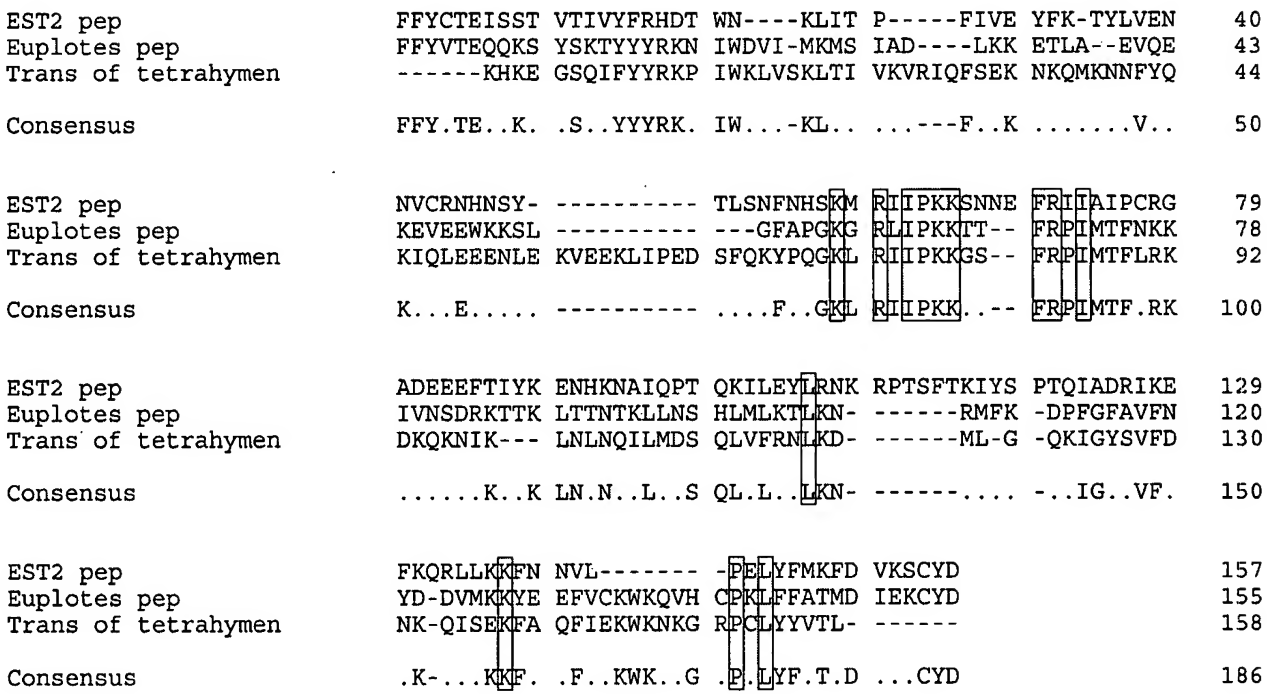

EST2 pep FFYCTEISST VTIVYFRHDT WN----KLIT P-----FIVE YFK-TYLVEN 40
Euplotes pep FFYVTEQQKS YSKTYYYRKN IWDVI-MKMS IAD----LKK ETLA--EVQE 43
Trans of tetrahymen ------KHKE GSQIFYYRKP IWKLVSKLTI VKVRIQFSEK NKQMKNNFYQ 44
Consensus FFY.TE..K. .S..YYYRK. IW...-KL.. .....-F..K .....V.. 50
EST2 pep NVCRNHNSY- ---------- TLSNFNHSKM RIIPKKSNNE FRIIAIPCRG 79
Euplotes pep KEVEEWKKSL ---------- ---GFAPGKG RLIPKKTT-- FRPIMTFNKK 78
Trans of tetrahymen KIQLEEENLE KVEEKLIPED SFQKYPQGKL RIIPKKGS-- FRPIMTFLRK 92
Consensus K...E..... ---------- ....F..GKL RIIPKK..-- FRPIMTF.RK 100
EST2 pep ADEEEFTIYK ENHKNAIQPT QKILEYLRNK RPTSFTKIYS PTQIADRIKE 129
Euplotes pep IVNSDRKTTK LTTNTKLLNS HLMLKTLKN- ------RMFK -DPFGFAVFN 120
Trans of tetrahymen DKQKNIK--- LNLNQILMDS QLVFRNLKD- ------ML-G -QKIGYSVFD 130
Consensus ......K..K LN.N..L..S QL.L..LKN- ---------- -..IG..VF. 150
EST2 pep FKQRLLKKFN NVL------- -PELYFMKFD VKSCYD 157
Euplotes pep YD-DVMKKYE EFVCKWKQVH CPKLFFATMD IEKCYD 155
Trans of tetrahymen NK-QISEKFA QFIEKWKNKG RPCLYYVTL- ------ 158
Consensus .K-...KKF. .F..KWK..G .P.LYF.T.D ...CYD 186

FIG. 31

```
S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE


A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV
```

FIG. 32

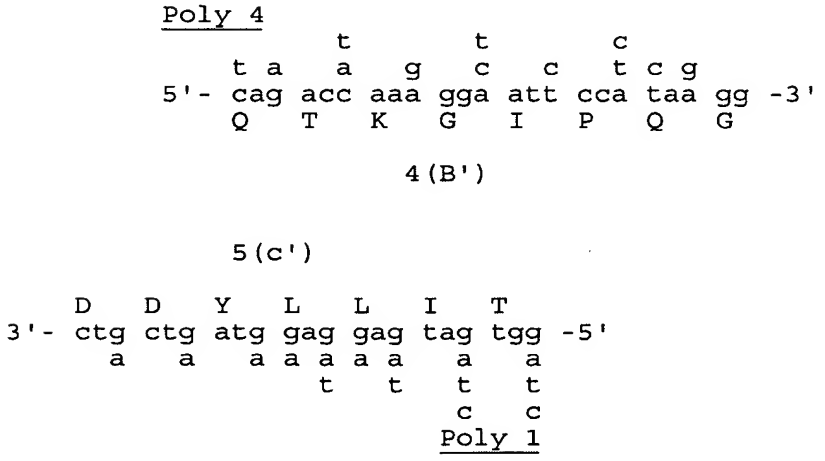


FIG. 34

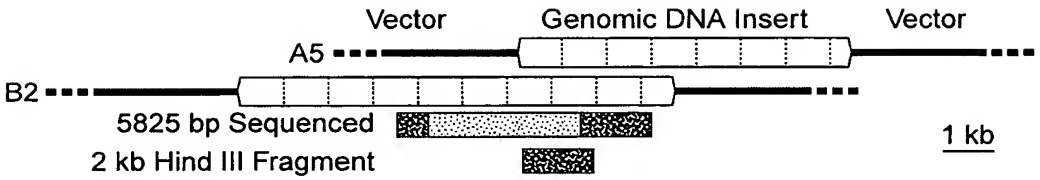


FIG. 33A

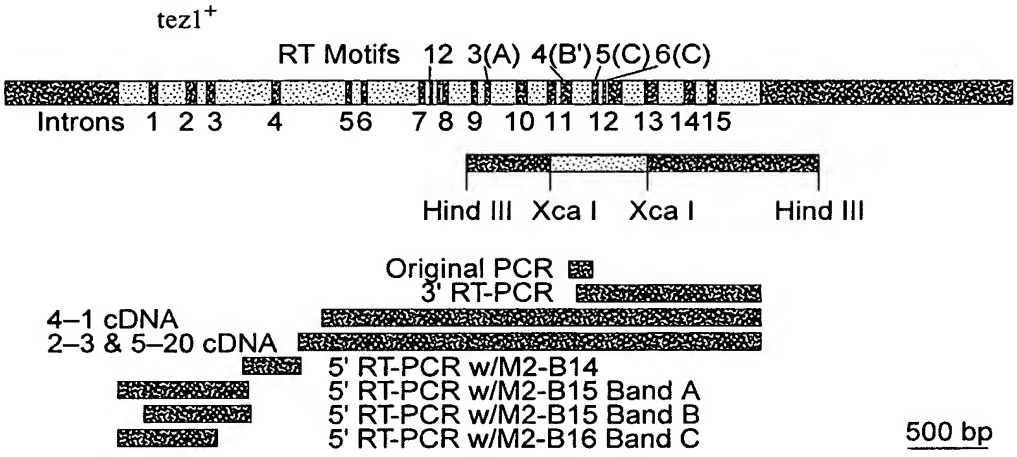


FIG. 33B

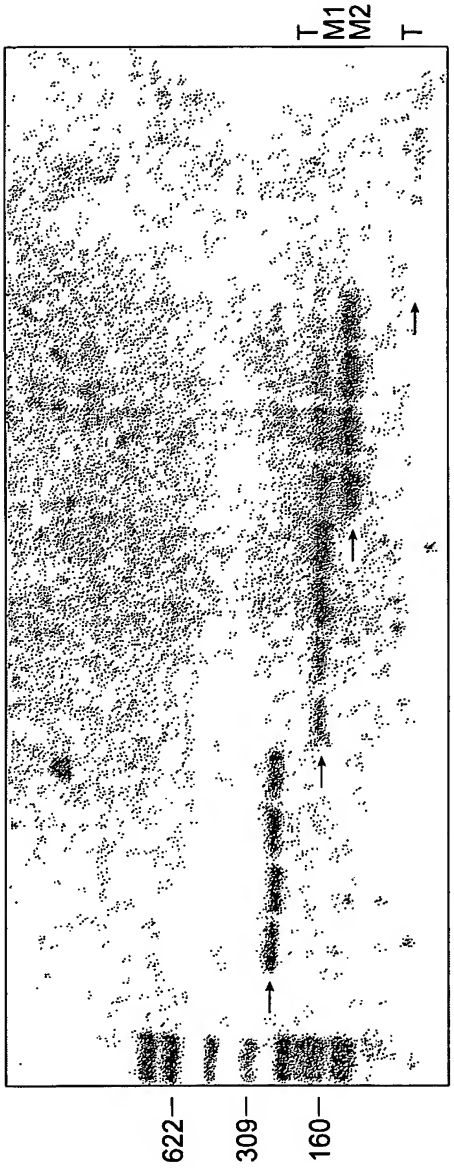


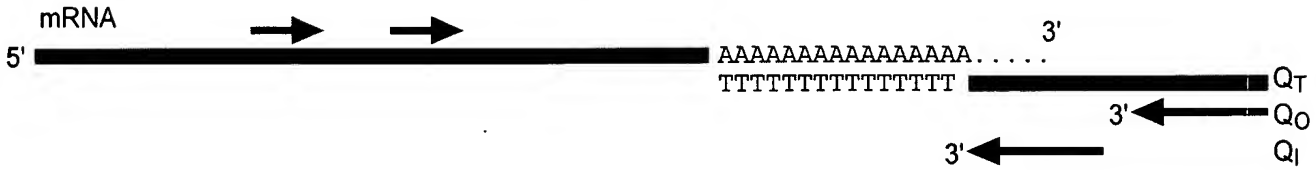
FIG. 35

```
Ot              LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123    KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2           SILSSFLCHFYMEDLIDEYLSFTKKK--------GSVLLRVV
Sc_p103    DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS------QDTLILKLADDFLIIS
                  .*  .       * .    *              .....


Q   K   V   G   I   P   Q   G
caa aaa gtt ggt atc cct cag gg......    <---Actual Genomic Sequence.

Poly 4
      t       t       c
t a   a   g   c   c   t c g
cag acc aaa gga att cca taa gg ---->

 ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
 tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

       K   G   I   P   S   G   S   I   L   S   S   F   L   C   H   F   Y   M
```

FIG. 36A

```
GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E   D   L   I   D   E   Y   L   S   F   T   K   K   K   G   S   V   L   L   R


GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

V   V   D   D   Y   L   L   I   T

  <---- ctg ctg atg gag gag tag tgg
          a   a   a a a a a   a   a
                    t   t   t   t
                            c   c
                          Poly 1

   .....gac gat ttc ctc ttt ata aca.....  <---Actual Genomic Sequence
        D   D   F   L   F   I   T
```

FIG. 36B



1. Synthesis of cDNA with Q_T Primer

2. First Round PCR Using Outside Primer and Q_O Primer

3. Second Round PCR Using Inside Primer and Q_I Primer

4. Sequence Second Round PCR Products Using Inside Primer Q_I Primer

FIG. 37

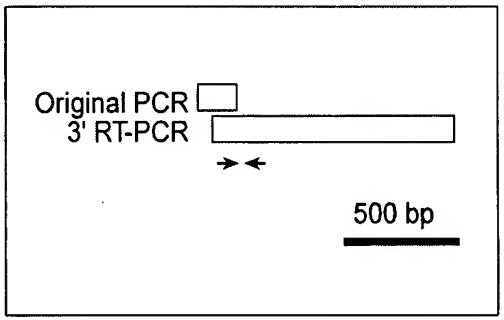
A. Genomic Libraries

Size Selected Libraries from P. Nurese
- 3~4 kb
- 5~7 kb
- 7~8 kb
- 11~12 kb

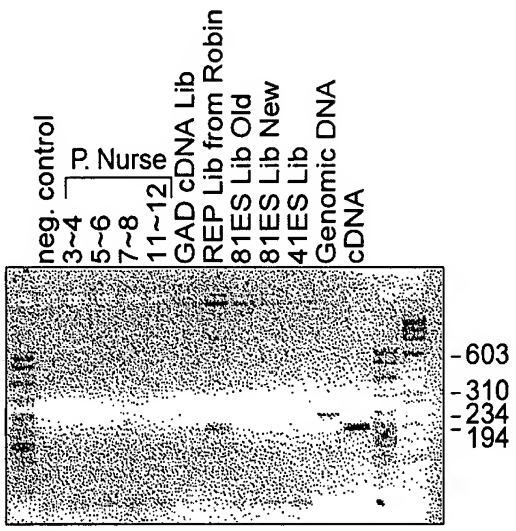
Libraries from J.A. Wise
- Sau 3a Partial Digest
- Hind III Partial Digest

cDNA Libraries
- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

B.



C.



D.

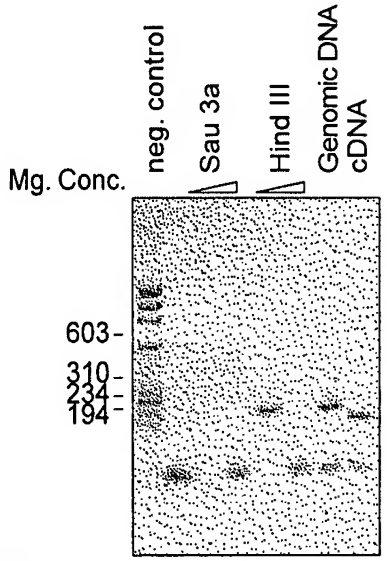


FIG. 38

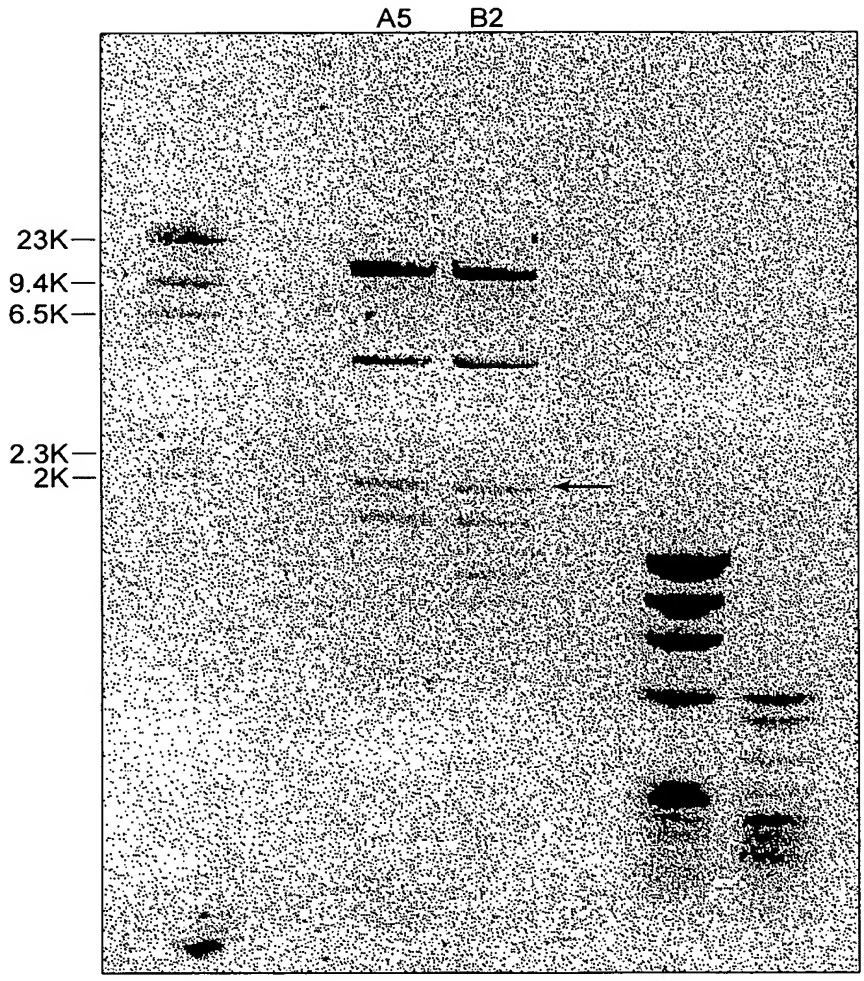


FIG. 39

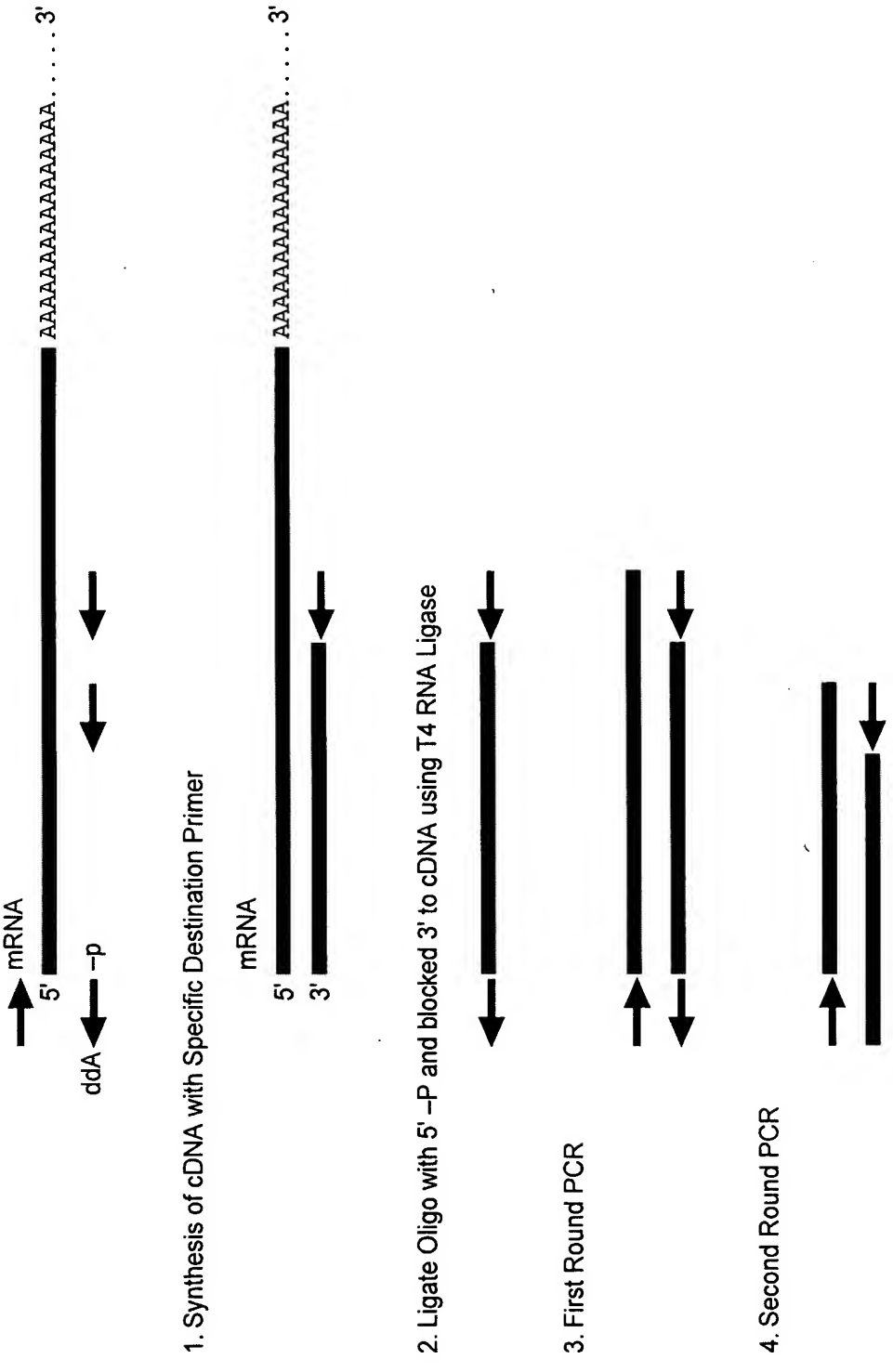

mRNA
5'
AAAAAAAAAAAAAAAAA.....3'
ddA
–p
1. Synthesis of cDNA with Specific Destination Primer
mRNA
5'
AAAAAAAAAAAAAAAAA.....3'
3'
2. Ligate Oligo with 5' –P and blocked 3' to cDNA using T4 RNA Ligase
3. First Round PCR
4. Second Round PCR

FIG. 40

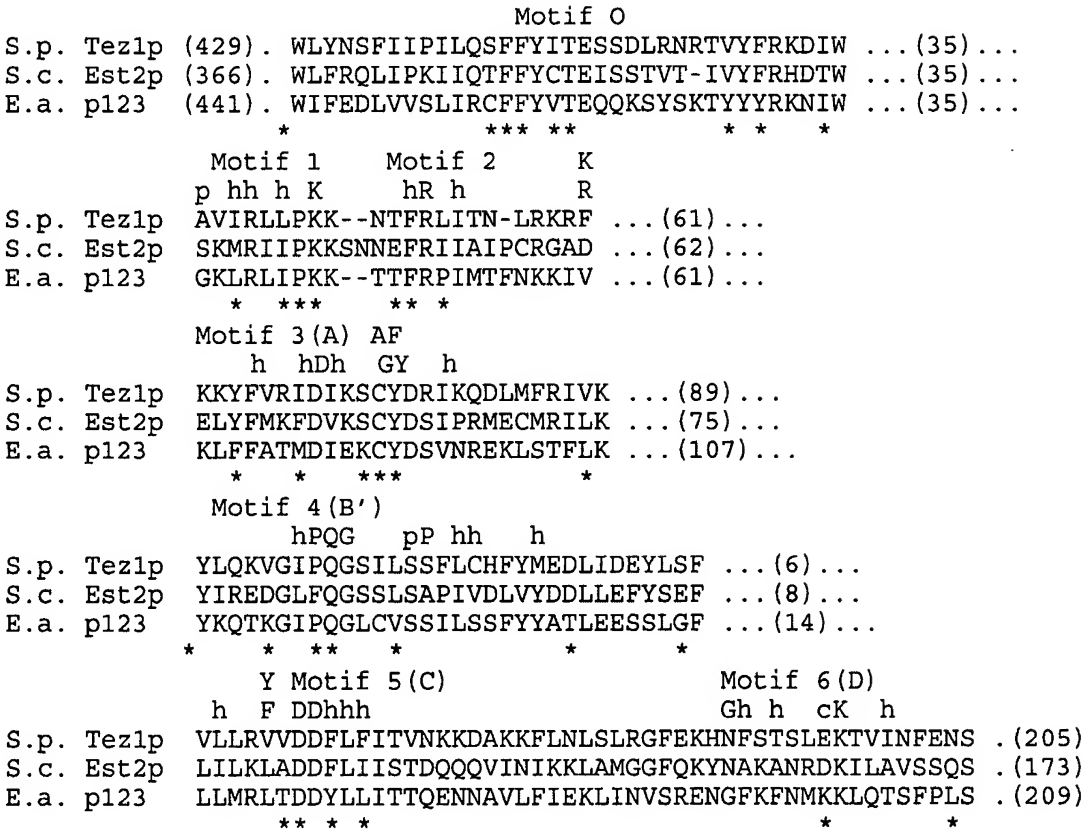

Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ...(35)...
S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ...(35)...
E.a. p123 (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ...(35)...
Motif 1
Motif 2
K
p hh h K
hR h
R
S.p. Tez1p AVIRLLPKK--NTFRLITN-LRKRF ...(61)...
S.c. Est2p SKMRIIPKKSNNEFRIIAIPCRGAD ...(62)...
E.a. p123 GKLRLIPKK--TTFRPIMTFNKKIV ...(61)...
Motif 3(A) AF
h hDh GY h
S.p. Tez1p KKYFVRIDIKSCYDRIKQDLMFRIVK ...(89)...
S.c. Est2p ELYFMKFDVKSCYDSIPRMECMRILK ...(75)...
E.a. p123 KLFFATMDIEKCYDSVNREKLSTFLK ...(107)...
Motif 4(B')
hPQG pP hh h
S.p. Tez1p YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ...(6)...
S.c. Est2p YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ...(8)...
E.a. p123 YKQTKGIPQGLCVSSILSSFYYATLEESSLGF ...(14)...
Y Motif 5(C)
Motif 6(D)
h F DDhhh
Gh h cK h
S.p. Tez1p VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS .(205)
S.c. Est2p LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS .(173)
E.a. p123 LLMRLTDDYLLITTQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLS .(209)

FIG. 41

A.

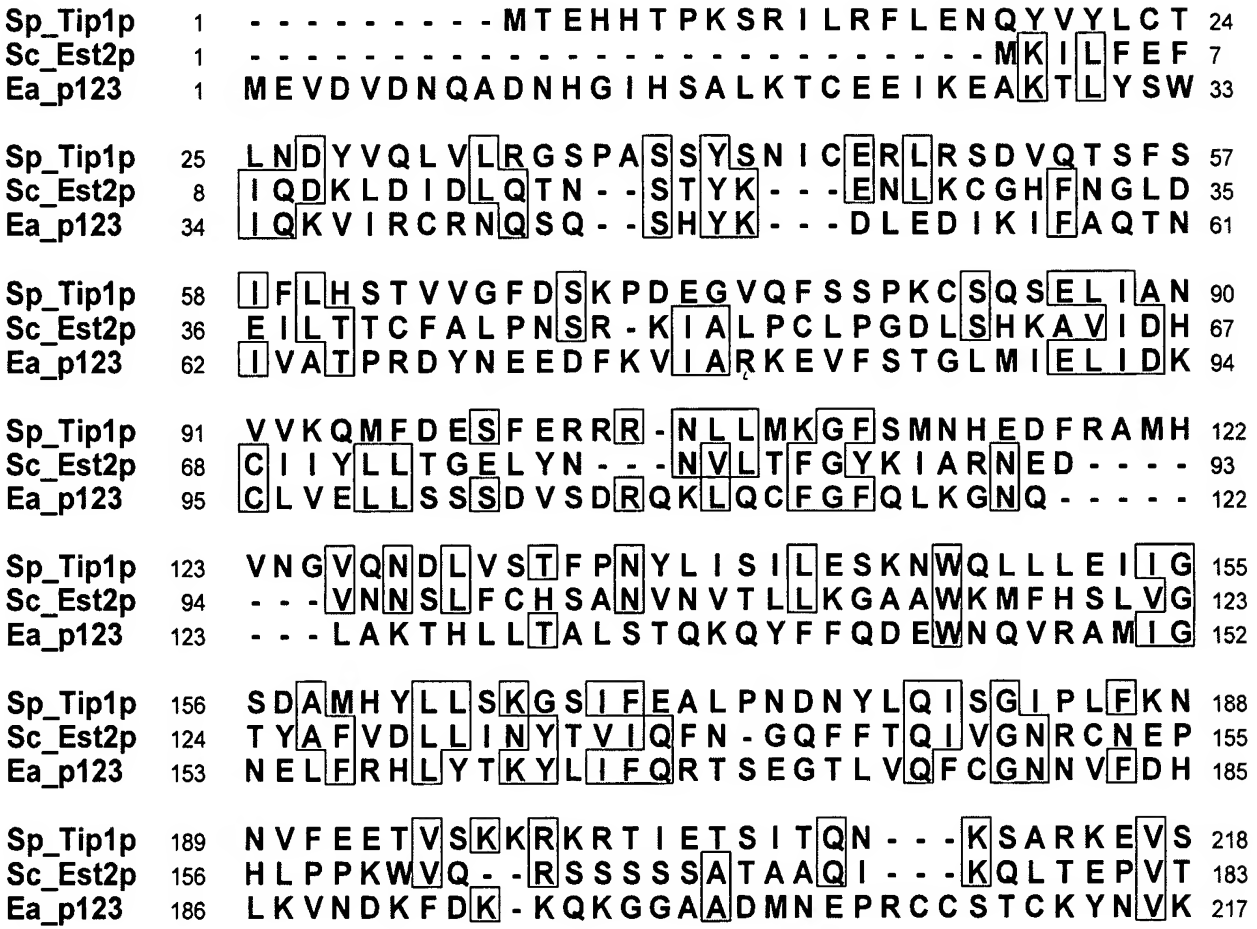

Sp_Tip1p 1 ----------MTEHHTPKSRILRFLENQYVYLCT 24
Sc_Est2p 1 ----------MKILFEF 7
Ea_p123 1 MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSW 33
Sp_Tip1p 25 LNDYVQLVLRGSPASSYSNICERLRSDVQTSFS 57
Sc_Est2p 8 IQDKLDIDLQTN--STYK---ENLKCGHFNGLD 35
Ea_p123 34 IQKVIRCRNQSQ--SHYK---DLEDIKIFAQTN 61
Sp_Tip1p 58 IFLHSTVVGFDSKPDEGVQFSSPKCSQSELIAN 90
Sc_Est2p 36 EILTTCFALPNSR-KIALPCLPGDLSHKAVIDH 67
Ea_p123 62 IVATPRDYNEEDFKVIARKEVFSTGLMIELIDK 94
Sp_Tip1p 91 VVKQMFDESFERRR-NLLMKGFSMNHEDFRAMH 122
Sc_Est2p 68 CIIYLLTGELYN---NVLTFGYKIARNED---- 93
Ea_p123 95 CLVELLSSSDVSDRQKLQCFGFQLKGNQ----- 122
Sp_Tip1p 123 VNGVQNDLVSTFPNYLISILESKNWQLLLEIIG 155
Sc_Est2p 94 ---VNNSLFCHSANVNVTLLKGAAWKMFHSLVG 123
Ea_p123 123 ---LAKTHLLTALSTQKQYFFQDEWNQVRAMIG 152
Sp_Tip1p 156 SDAMHYLLSKGSIFEALPNDNYLQISGIPLFKN 188
Sc_Est2p 124 TYAFVDLLINYTVIQFN-GQFFTQIVGNRCNEP 155
Ea_p123 153 NELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDH 185
Sp_Tip1p 189 NVFEETVSKKRKRTIETSITQN---KSARKEVS 218
Sc_Est2p 156 HLPPKWVQ--RSSSSSSATAAQI---KQLTEPVT 183
Ea_p123 186 LKVNDKFDK-KQKGGAADMNEPRCCSTCKYNVK 217

FIG. 42A

A.

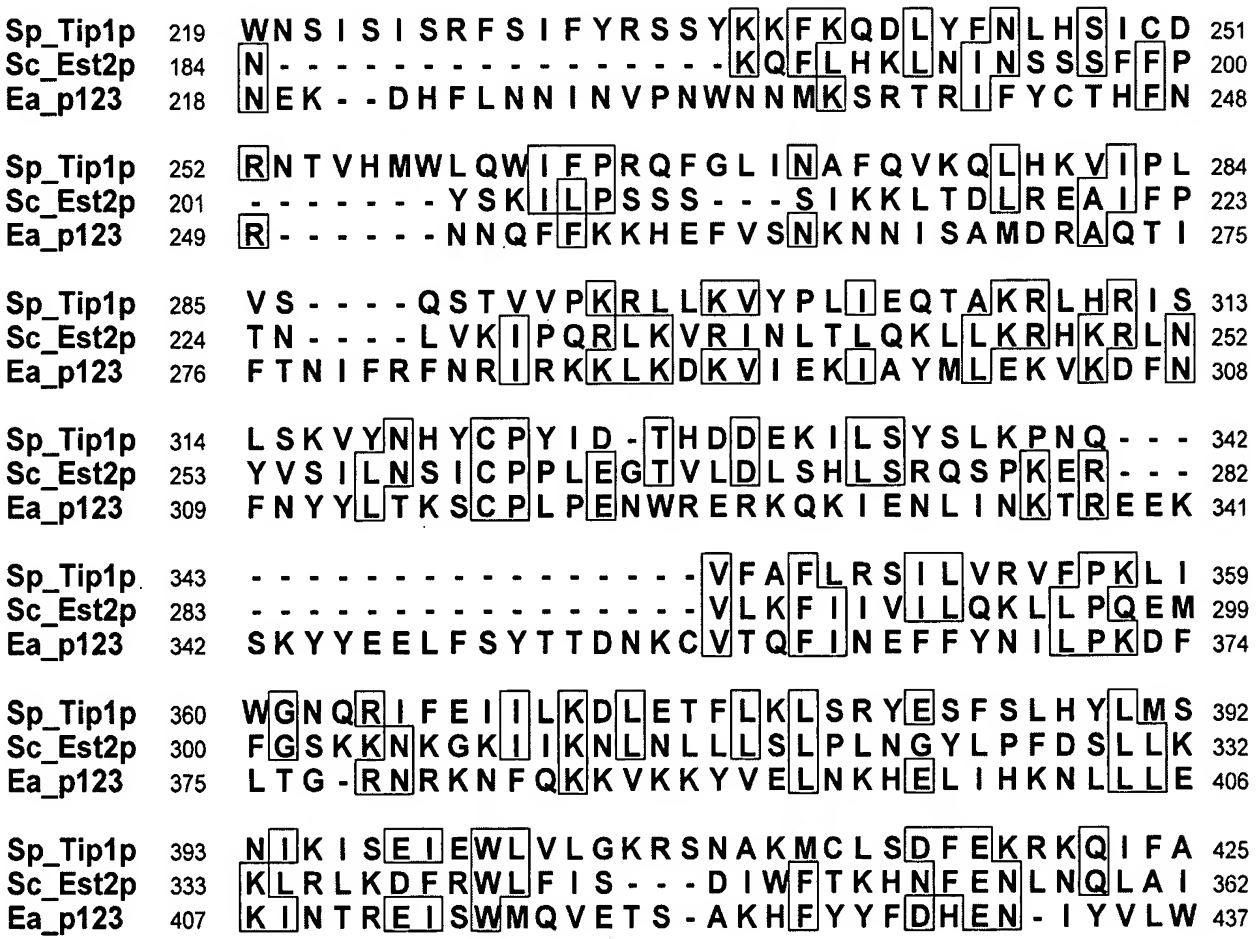

Sp_Tip1p 219 WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD 251
Sc_Est2p 184 N----------KQFLHKLNINSSSFFP 200
Ea_p123 218 NEK--DHFLNNINVPNWNNMKSRTRIFYCTHFN 248
Sp_Tip1p 252 RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL 284
Sc_Est2p 201 -------YSKILPSSS---SIKKLTDLREAIFP 223
Ea_p123 249 R------NNQFFKKHEFVSNKNNISAMDRAQTI 275
Sp_Tip1p 285 VS----QSTVVPKRLLKVYPLIEQTAKRLHRIS 313
Sc_Est2p 224 TN----LVKIPQRLKVRINLTLQKLLKRHKRLN 252
Ea_p123 276 FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN 308
Sp_Tip1p 314 LSKVYNHYCPYID-THDDEKILSYSLKPNQ--- 342
Sc_Est2p 253 YVSILNSICPPLEGTVLDLSHLSRQSPKER--- 282
Ea_p123 309 FNYYLTKSCPLPENWRERKQKIENLINKTREEK 341
Sp_Tip1p 343 ----------------VFAFLRSILVRVFPKLI 359
Sc_Est2p 283 ----------------VLKFIIVILQKLLPQEM 299
Ea_p123 342 SKYYEELFSYTTDNKCVTQFINEFFYNILPKDF 374
Sp_Tip1p 360 WGNQRIFEIILKDLETFLKLSRYESFSLHYLMS 392
Sc_Est2p 300 FGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLK 332
Ea_p123 375 LTG-RNRKNFQKKVKKYVELNKHELIHKNLLLE 406
Sp_Tip1p 393 NIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFA 425
Sc_Est2p 333 KLRLKDFRWLFIS---DIWFTKHNFENLNQLAI 362
Ea_p123 407 KINTREISWMQVETS-AKHFYYFDHEN-IYVLW 437

FIG. 42B

A.

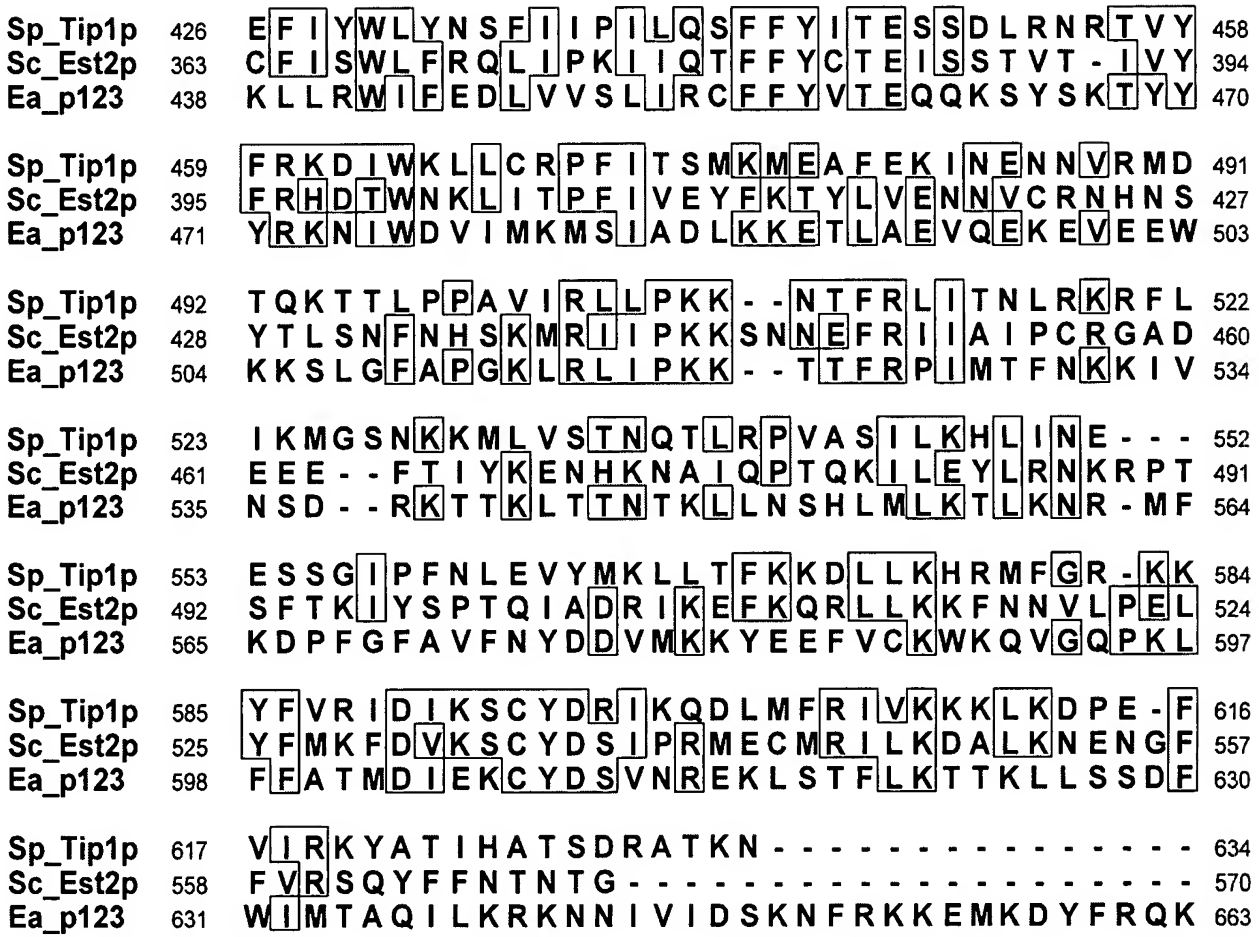

Sp_Tip1p 426 EFIYWLYNSFIIPILQSFFYITESSDLRNRTVY 458
Sc_Est2p 363 CFISWLFRQLIPKIIQTFFYCTEISSTVT-IVY 394
Ea_p123 438 KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYY 470
Sp_Tip1p 459 FRKDIWKLLCRPFITSMKMEAFEKINENNVRMD 491
Sc_Est2p 395 FRHDTWNKLITPFIVEYFKTYLVENNVCRNHNS 427
Ea_p123 471 YRKNIWDVIMKMSIADLKKETLAEVQEKEVEEW 503
Sp_Tip1p 492 TQKTTLPPAVIRLLPKK--NTFRLITNLRKRFL 522
Sc_Est2p 428 YTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD 460
Ea_p123 504 KKSLGFAPGKLRLIPKK--TTFRPIMTFNKKIV 534
Sp_Tip1p 523 IKMGSNKKMLVSTNQTLRPVASILKHLINE--- 552
Sc_Est2p 461 EEE--FTIYKENHKNAIQPTQKILEYLRNKRPT 491
Ea_p123 535 NSD--RKTTKLTTNTKLLNSHLMLKTLKNR-MF 564
Sp_Tip1p 553 ESSGIPFNLEVYMKLLTFKKDLLKHRMFGR-KK 584
Sc_Est2p 492 SFTKIYSPTQIADRIKEFKQRLLKKFNNVLPEL 524
Ea_p123 565 KDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL 597
Sp_Tip1p 585 YFVRIDIKSCYDRIKQDLMFRIVKKKLKDPE-F 616
Sc_Est2p 525 YFMKFDVKSCYDSIPRMECMRILKDALKNENGF 557
Ea_p123 598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDF 630
Sp_Tip1p 617 VIRKYATIHATSDRATKN---------------- 634
Sc_Est2p 558 FVRSQYFFNTNTG---------------------- 570
Ea_p123 631 WIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQK 663

FIG. 42C

A.

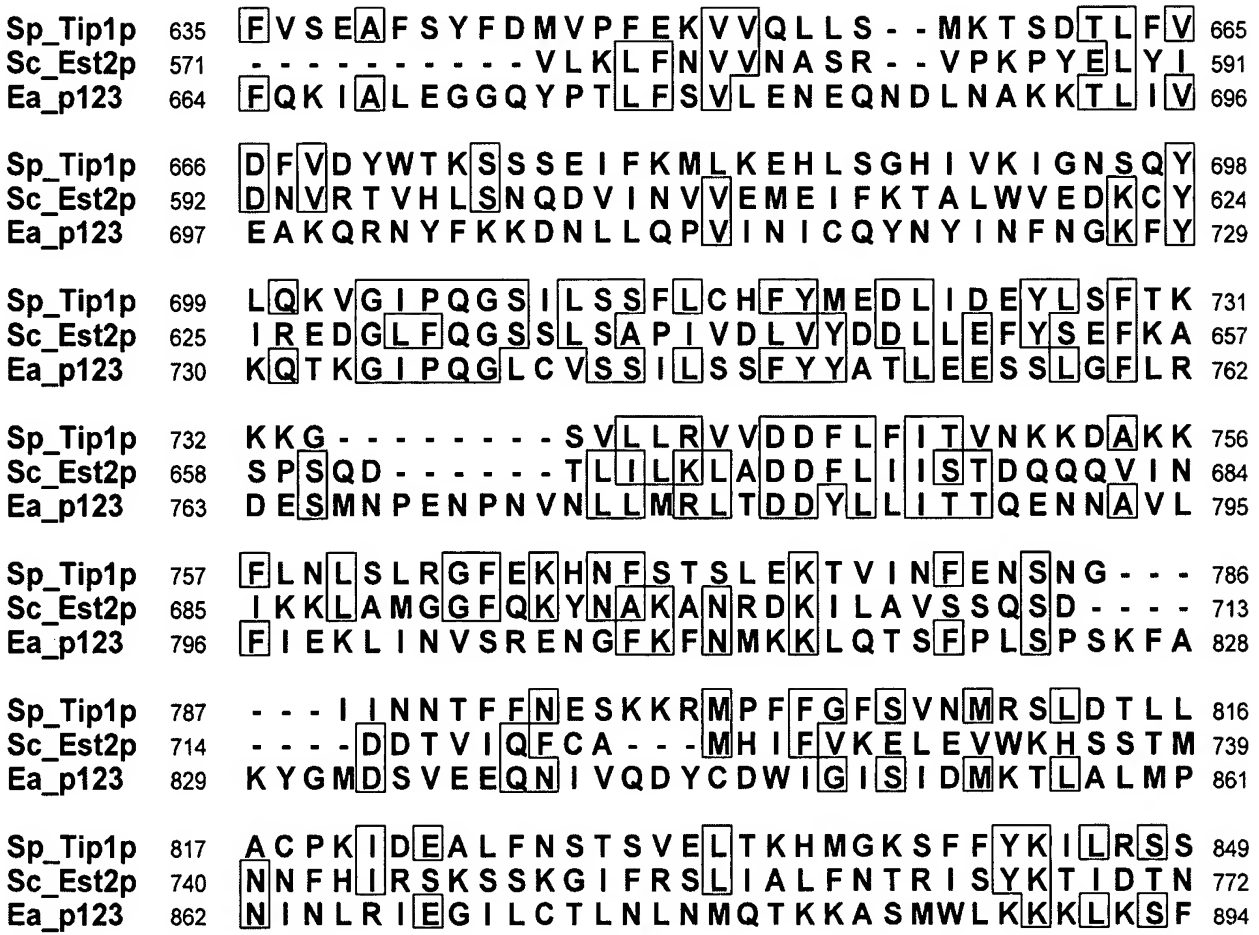

Sp_Tip1p 635 FVSEAFSYFDMVPFEKVVQLLS--MKTSDTLFV 665
Sc_Est2p 571 ----------VLKLFNVVNASR--VPKPYELYI 591
Ea_p123 664 FQKIALEGGQYPTLFSVLENEQNDLNAKKTLIV 696
Sp_Tip1p 666 DFVDYWTKSSSEIFKMLKEHLSGHIVKIGNSQY 698
Sc_Est2p 592 DNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY 624
Ea_p123 697 EAKQRNYFKKDNLLQPVINICQYNYINFNGKFY 729
Sp_Tip1p 699 LQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTK 731
Sc_Est2p 625 IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKA 657
Ea_p123 730 KQTKGIPQGLCVSSILSSFYYATLEESSLGFLR 762
Sp_Tip1p 732 KKG---------SVLLRVVDDFLFITVNKKDAKK 756
Sc_Est2p 658 SPSQD------TLILKLADDFLIISTDQQQVIN 684
Ea_p123 763 DESMNPENPNVNLLMRLTDDYLLITTQENNAVL 795
Sp_Tip1p 757 FLNLSLRGFEKHNFSTSLEKTVINFENSNG--- 786
Sc_Est2p 685 IKKLAMGGFQKYNAKANRDKILAVSSQSD---- 713
Ea_p123 796 FIEKLINVSRENGFKFNMKKLQTSFPLSPSKFA 828
Sp_Tip1p 787 ---IINNTFFNESKKRMPFFGFSVNMRSLDTLL 816
Sc_Est2p 714 ----DDTVIQFCA---MHIFVKELEVWKHSSTM 739
Ea_p123 829 KYGMDSVEEQNIVQDYCDWIGISIDMKTLALMP 861
Sp_Tip1p 817 ACPKIDEALFNSTSVELTKHMGKSFFYKILRSS 849
Sc_Est2p 740 NNFHIRSKSSKGIFRSLIALFNTRISYKTIDTN 772
Ea_p123 862 NINLRIEGILCTLNLNMQTKKASMWLKKKLKSF 894

FIG. 42D

A.

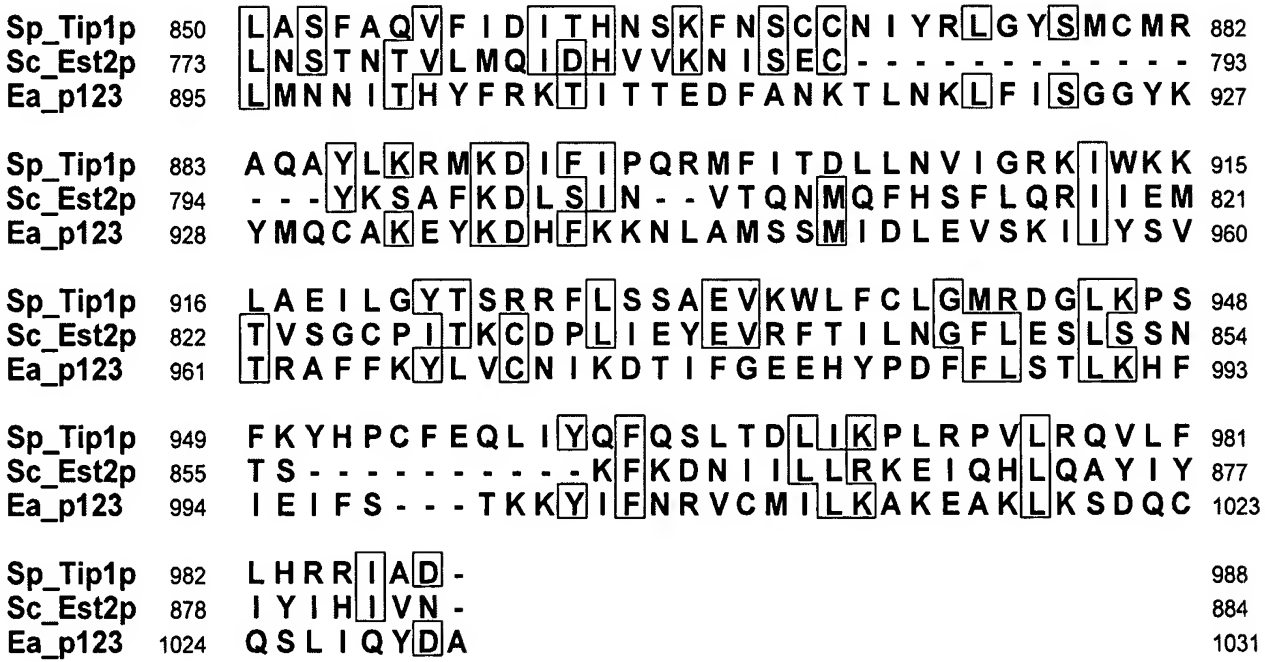

Sp_Tip1p 850 LASFAQVFIDITHNSKFNSCCNIYRLGYSMCMR 882
Sc_Est2p 773 LNSTNTVLMQIDHVVKNISEC---------- 793
Ea_p123 895 LMNNITHYFRKTITTEDFANKTLNKLFISGGYK 927
Sp_Tip1p 883 AQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKK 915
Sc_Est2p 794 ---YKSAFKDLSIN--VTQNMQFHSFLQRIIEM 821
Ea_p123 928 YMQCAKEYKDHFKKNLAMSSMIDLEVSKIIYSV 960
Sp_Tip1p 916 LAEILGYTSRRFLSSAEVKWLFCLGMRDGLKPS 948
Sc_Est2p 822 TVSGCPITKCDPLIEYEVRFTILNGFLESLSSN 854
Ea_p123 961 TRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHF 993
Sp_Tip1p 949 FKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF 981
Sc_Est2p 855 TS----------KFKDNIILLRKEIQHLQAYIY 877
Ea_p123 994 IEIFS---TKKYIFNRVCMILKAKEAKLKSDQC 1023
Sp_Tip1p 982 LHRRIAD- 988
Sc_Est2p 878 IYIHIVN- 884
Ea_p123 1024 QSLIQYDA 1031

FIG. 42E

B.

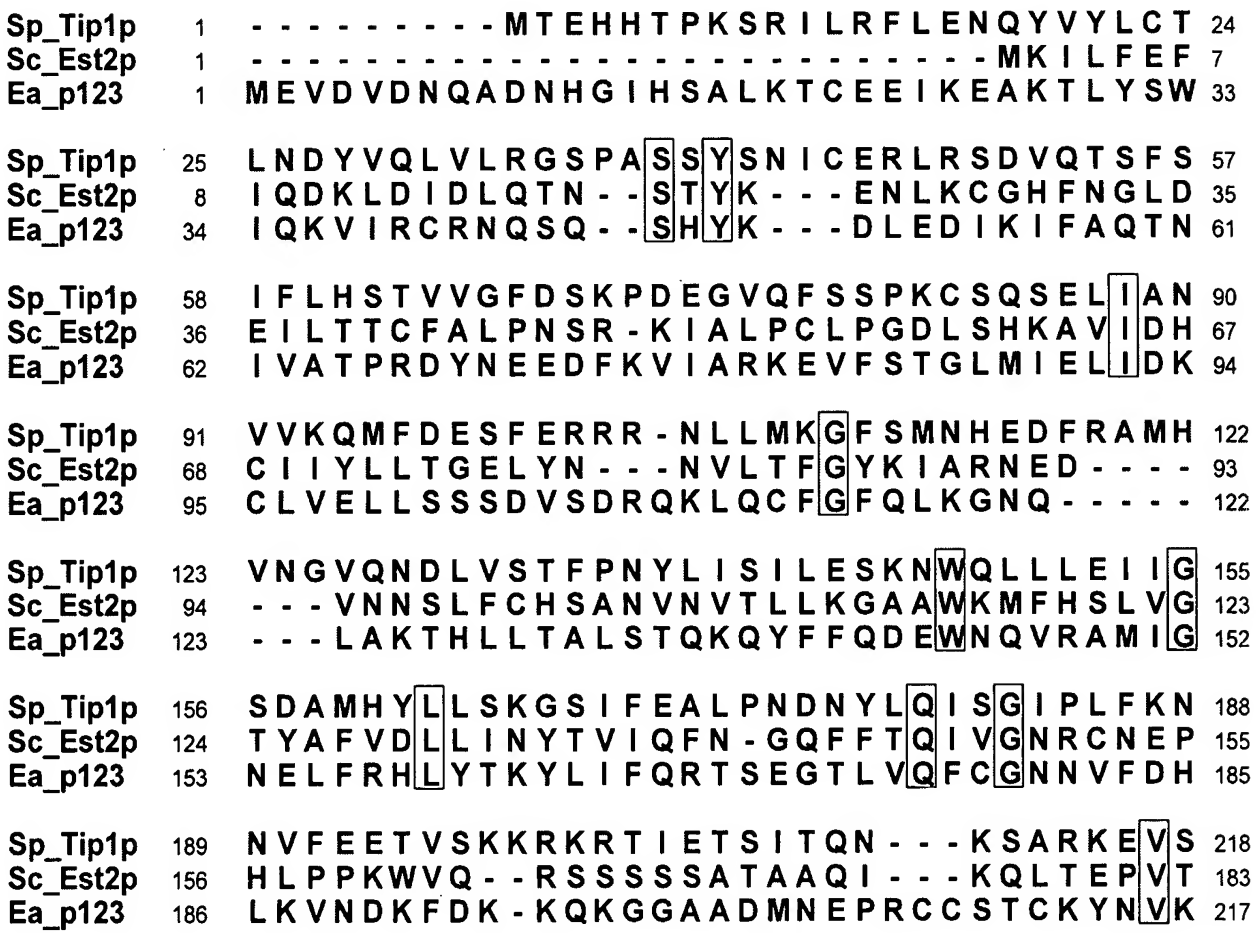

Sp_Tip1p 1 ----------MTEHHTPKSRILRFLENQYVYLCT 24
Sc_Est2p 1 ----------MKILFEF 7
Ea_p123 1 MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSW 33
Sp_Tip1p 25 LNDYVQLVLRGSPASSYSNICERLRSDVQTSFS 57
Sc_Est2p 8 IQDKLDIDLQTN--STYK---ENLKCGHFNGLD 35
Ea_p123 34 IQKVIRCRNQSQ--SHYK---DLEDIKIFAQTN 61
Sp_Tip1p 58 IFLHSTVVGFDSKPDEGVQFSSPKCSQSELIAN 90
Sc_Est2p 36 EILTTCFALPNSR-KIALPCLPGDLSHKAVIDH 67
Ea_p123 62 IVATPRDYNEEDFKVIARKEVFSTGLMIELIDK 94
Sp_Tip1p 91 VVKQMFDESFERRR-NLLMKGFSMNHEDFRAMH 122
Sc_Est2p 68 CIIYLLTGELYN---NVLTFGYKIARNED---- 93
Ea_p123 95 CLVELLSSSDVSDRQKLQCFGFQLKGNQ----- 122
Sp_Tip1p 123 VNGVQNDLVSTFPNYLISILESKNWQLLLEIIG 155
Sc_Est2p 94 ---VNNSLFCHSANVNVTLLKGAAWKMFHSLVG 123
Ea_p123 123 ---LAKTHLLTALSTQKQYFFQDEWNQVRAMIG 152
Sp_Tip1p 156 SDAMHYLLSKGSIFEALPNDNYLQISGIPLFKN 188
Sc_Est2p 124 TYAFVDLLINYTVIQFN-GQFFTQIVGNRCNEP 155
Ea_p123 153 NELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDH 185
Sp_Tip1p 189 NVFEETVSKKRKRTIETSITQN---KSARKEVS 218
Sc_Est2p 156 HLPPKWVQ--RSSSSSSATAAQI---KQLTEPVT 183
Ea_p123 186 LKVNDKFDK-KQKGGAADMNEPRCCSTCKYNVK 217

FIG. 42F

B.

```
Sp_Tip1p  219  WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD  251
Sc_Est2p  184  N----------------KQFLHKLNINSSSFFP  200
Ea_p123   218  NEK--DHFLNNINVPNWNNMKSRTRIFYCTHFN  248

Sp_Tip1p  252  RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL  284
Sc_Est2p  201  -------YSKILPSSS---SIKKLTDLREAIFP  223
Ea_p123   249  R------NNQFFKKHEFVSNKNNISAMDRAQTI  275

Sp_Tip1p  285  VS----QSTVVPKRLLKVYPLIEQTAKRLHRIS  313
Sc_Est2p  224  TN----LVKIPQRLKVRINLTLQKLLKRHKRLN  252
Ea_p123   276  FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN  308

Sp_Tip1p  314  LSKVYNHYCPYID-THDDEKILSYSLKPNQ---  342
Sc_Est2p  253  YVSILNSICPPLEGTVLDLSHLSRQSPKER---  282
Ea_p123   309  FNYYLTKSCPLPENWRERKQKIENLINKTREEK  341

Sp_Tip1p  343  ----------------VFAFLRSILVRVFPKLI  359
Sc_Est2p  283  ----------------VLKFIIVILQKLLPQEM  299
Ea_p123   342  SKYYEELFSYTTDNKCVTQFINEFFYNILPKDF  374

Sp_Tip1p  360  WGNQRIFEIILKDLETFLKLSRYESFSLHYLMS  392
Sc_Est2p  300  FGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLK  332
Ea_p123   375  LTG-RNRKNFQKKVKKYVELNKHELIHKNLLLE  406

Sp_Tip1p  393  NIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFA  425
Sc_Est2p  333  KLRLKDFRWLFIS---DIWFTKHNFENLNQLAI  362
Ea_p123   407  KINTREISWMQVETS-AKHFYYFDHEN-IYVLW  437
```

FIG. 42G

B.

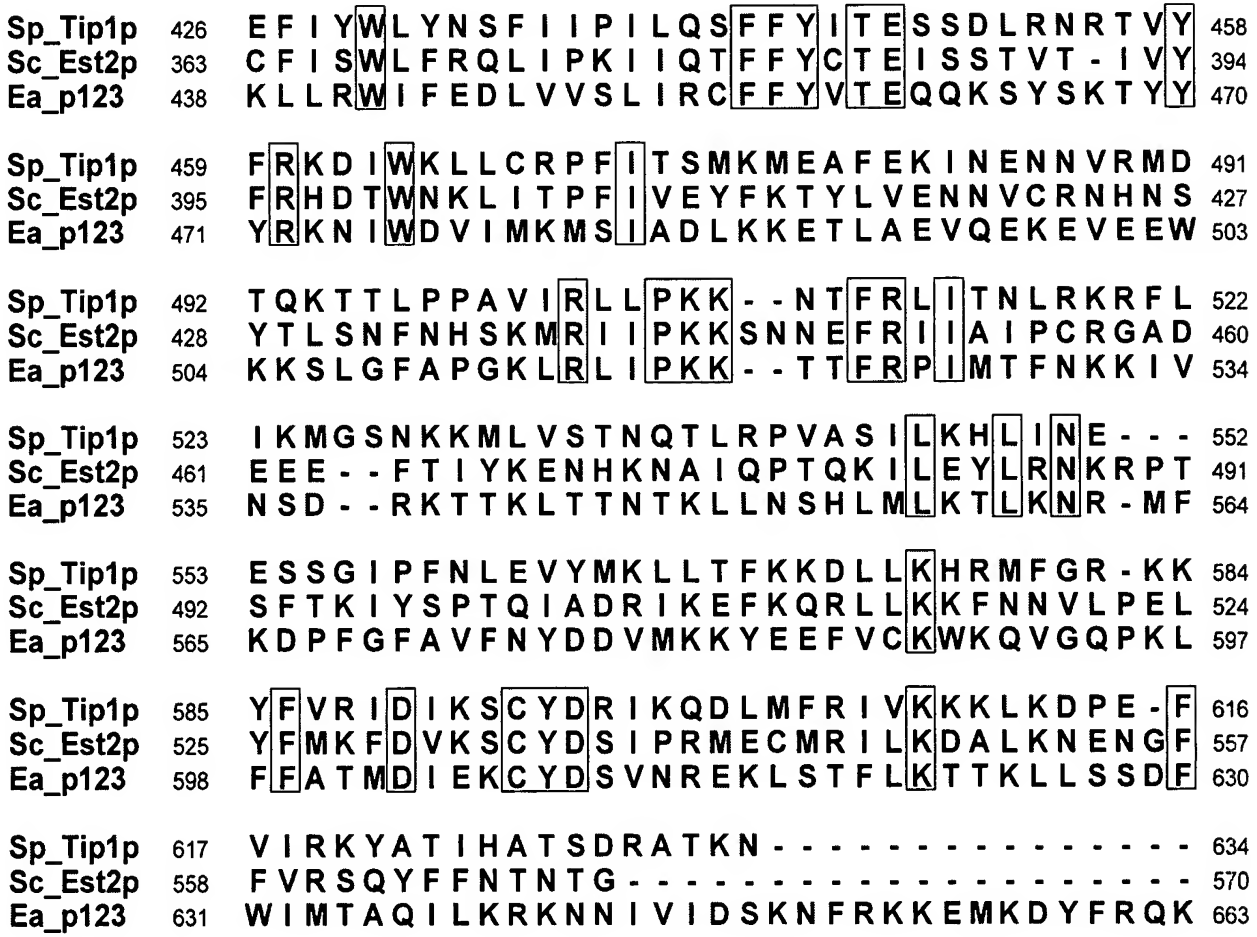

Sp_Tip1p 426 EFIYWLYNSFIIPILQSFFYITESSDLRNRTVY 458
Sc_Est2p 363 CFISWLFRQLIPKIIQTFFYCTEISSTVT-IVY 394
Ea_p123 438 KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYY 470
Sp_Tip1p 459 FRKDIWKLLCRPFITSMKMEAFEKINENNVRMD 491
Sc_Est2p 395 FRHDTWNKLITPFIVEYFKTYLVENNVCRNHNS 427
Ea_p123 471 YRKNIWDVIMKMSIADLKKETLAEVQEKEVEEW 503
Sp_Tip1p 492 TQKTTLPPAVIRLLPKK--NTFRLITNLRKRFL 522
Sc_Est2p 428 YTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD 460
Ea_p123 504 KKSLGFAPGKLRLIPKK--TTFRPIMTFNKKIV 534
Sp_Tip1p 523 IKMGSNKKMLVSTNQTLRPVASILKHLINE--- 552
Sc_Est2p 461 EEE--FTIYKENHKNAIQPTQKILEYLRNKRPT 491
Ea_p123 535 NSD--RKTTKLTTNTKLLNSHLMLKTLKNR-MF 564
Sp_Tip1p 553 ESSGIPFNLEVYMKLLTFKKDLLKHRMFGR-KK 584
Sc_Est2p 492 SFTKIYSPTQIADRIKEFKQRLLKKFNNVLPEL 524
Ea_p123 565 KDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL 597
Sp_Tip1p 585 YFVRIDIKSCYDRIKQDLMFRIVKKKLKDPE-F 616
Sc_Est2p 525 YFMKFDVKSCYDSIPRMECMRILKDALKNENGF 557
Ea_p123 598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDF 630
Sp_Tip1p 617 VIRKYATIHATSDRATKN---------- 634
Sc_Est2p 558 FVRSQYFFNTNTG---------- 570
Ea_p123 631 WIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQK 663

FIG. 42H

B.

```
Sp_Tip1p  635  FVSEAFSYFDMVPFEKVVQLLS--MKTSDTLFV  665
Sc_Est2p  571  ----------VLKLFNVVNASR--VPKPYELYI  591
Ea_p123   664  FQKIALEGGQYPTLFSVLENEQNDLNAKKTLIV  696

Sp_Tip1p  666  DFVDYWTKSSSEIFKMLKEHLSGHIVKIGNSQY  698
Sc_Est2p  592  DNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY  624
Ea_p123   697  EAKQRNYFKKDNLLQPVINICQYNYINFNGKFY  729

Sp_Tip1p  699  LQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTK  731
Sc_Est2p  625  IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKA  657
Ea_p123   730  KQTKGIPQGLCVSSILSSFYYATLEESSLGFLR  762

Sp_Tip1p  732  KKG--------SVLLRVVDDFLFITVNKKDAKK  756
Sc_Est2p  658  SPSQD------TLILKLADDFLIISTDQQQVIN  684
Ea_p123   763  DESMNPENPNVNLLMRLTDDYLLITTQENNAVL  795

Sp_Tip1p  757  FLNLSLRGFEKHNFSTSLEKTVINFENSNG---  786
Sc_Est2p  685  IKKLAMGGFQKYNAKANRDKILAVSSQSD----  713
Ea_p123   796  FIEKLINVSRENGFKFNMKKLQTSFPLSPSKFA  828

Sp_Tip1p  787  ---IINNTFFNESKKRMPFFGFSVNMRSLDTLL  816
Sc_Est2p  714  ----DDTVIQFCA---MHIFVKELEVWKHSSTM  739
Ea_p123   829  KYGMDSVEEQNIVQDYCDWIGISIDMKTLALMP  861

Sp_Tip1p  817  ACPKIDEALFNSTSVELTKHMGKSFFYKILRSS  849
Sc_Est2p  740  NNFHIRSKSSKGIFRSLIALFNTRISYKTIDTN  772
Ea_p123   862  NINLRIEGILCTLNLNMQTKKASMWLKKKLKSF  894
```

FIG. 42I

B.

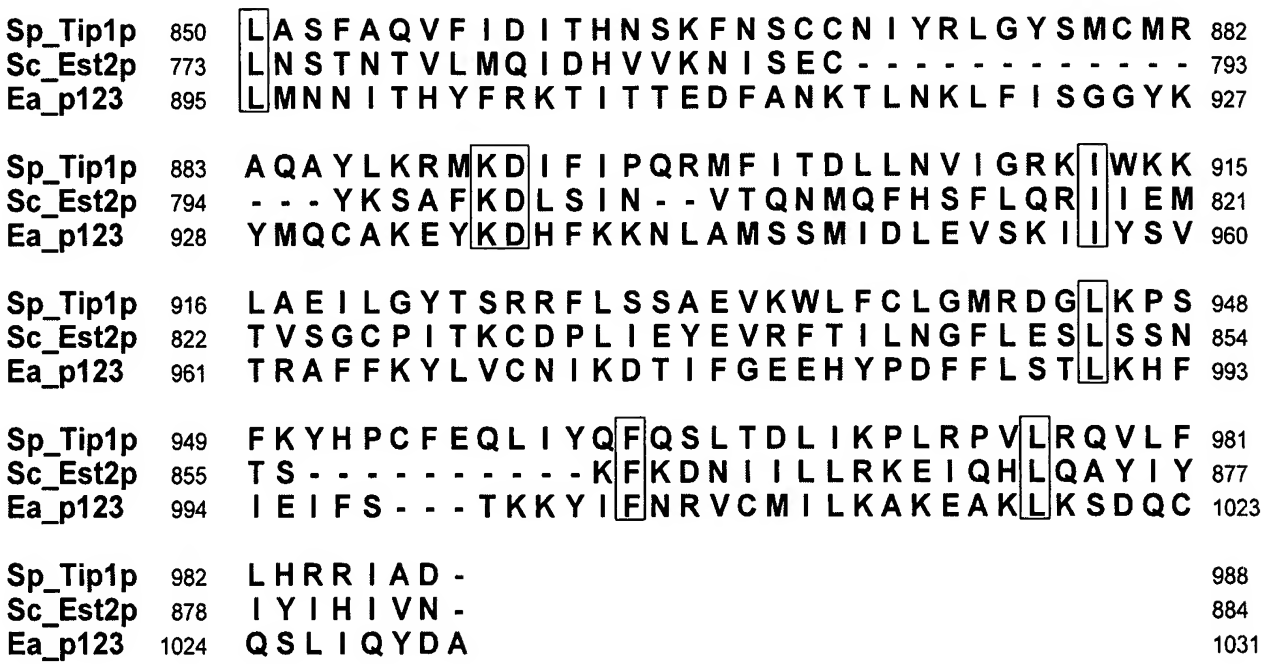

Sp_Tip1p 850 LASFAQVFIDITHNSKFNSCCNIYRLGYSMCMR 882
Sc_Est2p 773 LNSTNTVLMQIDHVVKNISEC-------------- 793
Ea_p123 895 LMNNITHYFRKTITTEDFANKTLNKLFISGGYK 927
Sp_Tip1p 883 AQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKK 915
Sc_Est2p 794 ---YKSAFKDLSIN--VTQNMQFHSFLQRIIEM 821
Ea_p123 928 YMQCAKEYKDHFKKNLAMSSMIDLEVSKIIYSV 960
Sp_Tip1p 916 LAEILGYTSRRFLSSAEVKWLFCLGMRDGLKPS 948
Sc_Est2p 822 TVSGCPITKCDPLIEYEVRFTILNGFLESLSSN 854
Ea_p123 961 TRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHF 993
Sp_Tip1p 949 FKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF 981
Sc_Est2p 855 TS----------KFKDNIILLRKEIQHLQAYIY 877
Ea_p123 994 IEIFS---TKKYIFNRVCMILKAKEAKLKSDQC 1023
Sp_Tip1p 982 LHRRIAD- 988
Sc_Est2p 878 IYIHIVN- 884
Ea_p123 1024 QSLIQYDA 1031

FIG. 42J

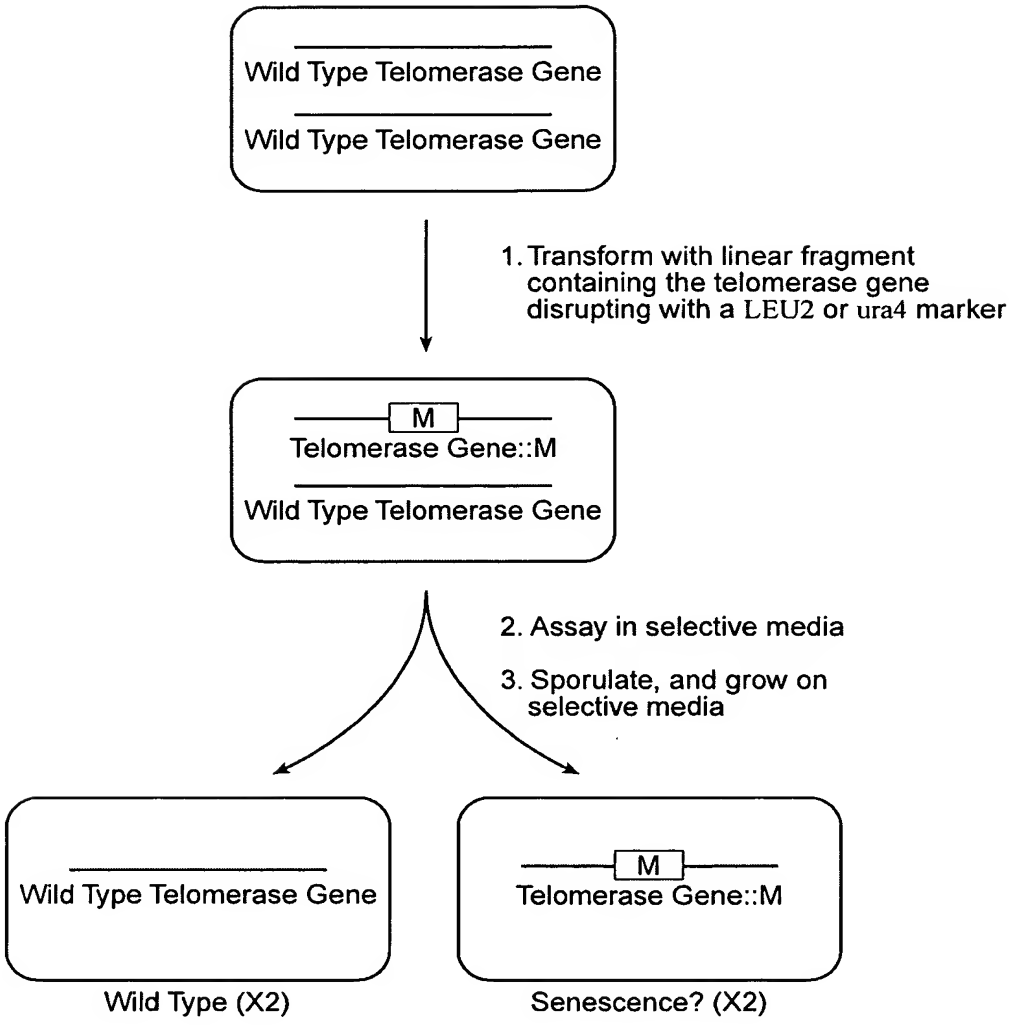

Wild Type Telomerase Gene
Wild Type Telomerase Gene
1. Transform with linear fragment containing the telomerase gene disrupting with a LEU2 or ura4 marker
M
Telomerase Gene::M
Wild Type Telomerase Gene
2. Assay in selective media
3. Sporulate, and grow on selective media
Wild Type Telomerase Gene
Wild Type (X2)
M
Telomerase Gene::M
Senescence? (X2)
(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIG. 43

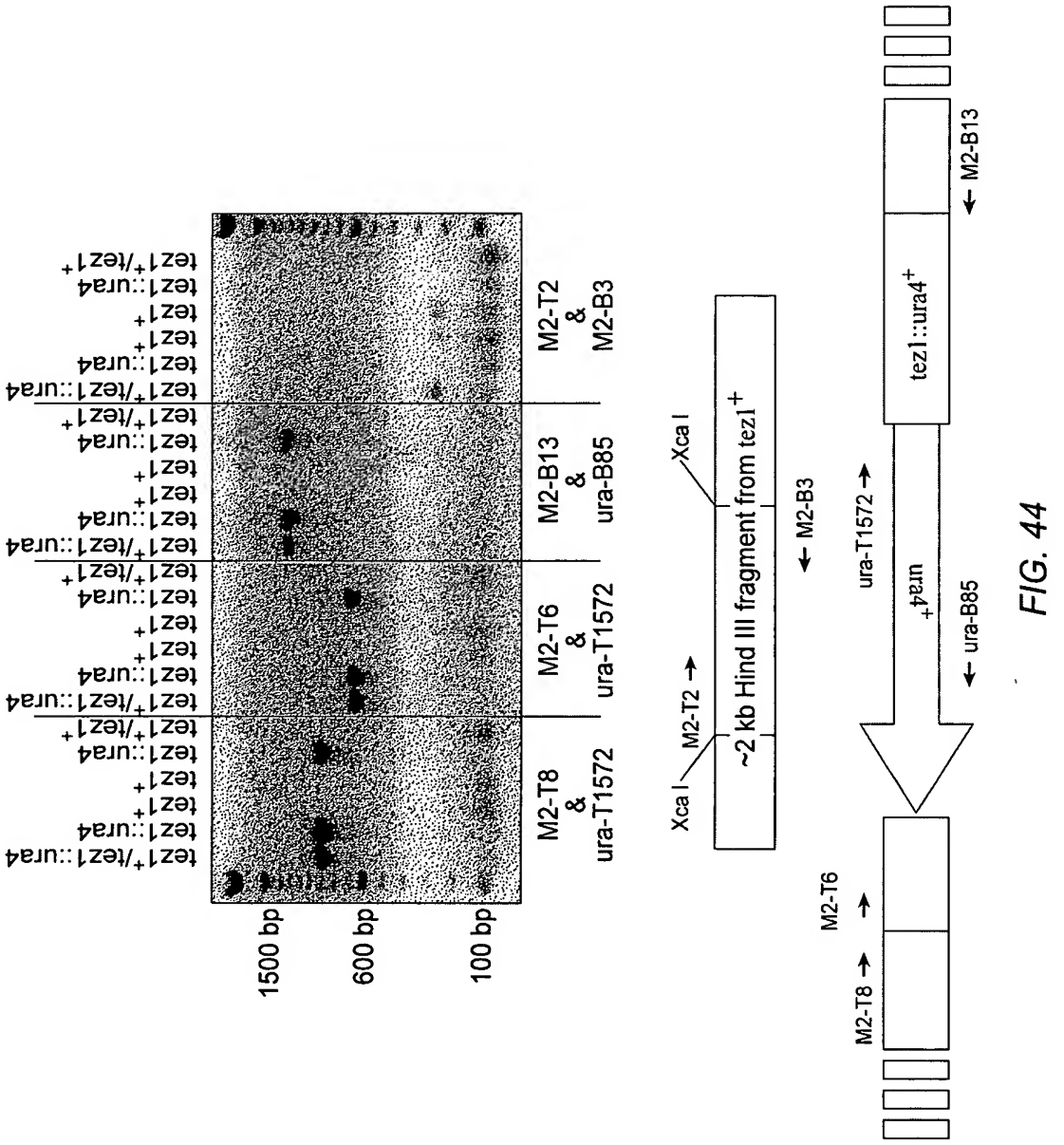

1500 bp
600 bp
100 bp
M2-T8 & ura-T1572
M2-T6 & ura-T1572
M2-B13 & ura-B85
M2-T2 & M2-B3
tez1+/tez1+
tez1::ura4
tez1+
tez1+
tez1::ura4
tez1+/tez1+
tez1+/tez1::ura4
tez1+
tez1+
tez1::ura4
tez1+/tez1+
tez1+/tez1::ura4
tez1+
tez1+
tez1::ura4
tez1+/tez1+
tez1+/tez1::ura4
Xca I
M2-T2
~2 kb Hind III fragment from tez1+
Xca I
M2-B3
M2-T6
M2-T8
ura-T1572
ura4+
tez1::ura4+
M2-B13
ura-B85

FIG. 44

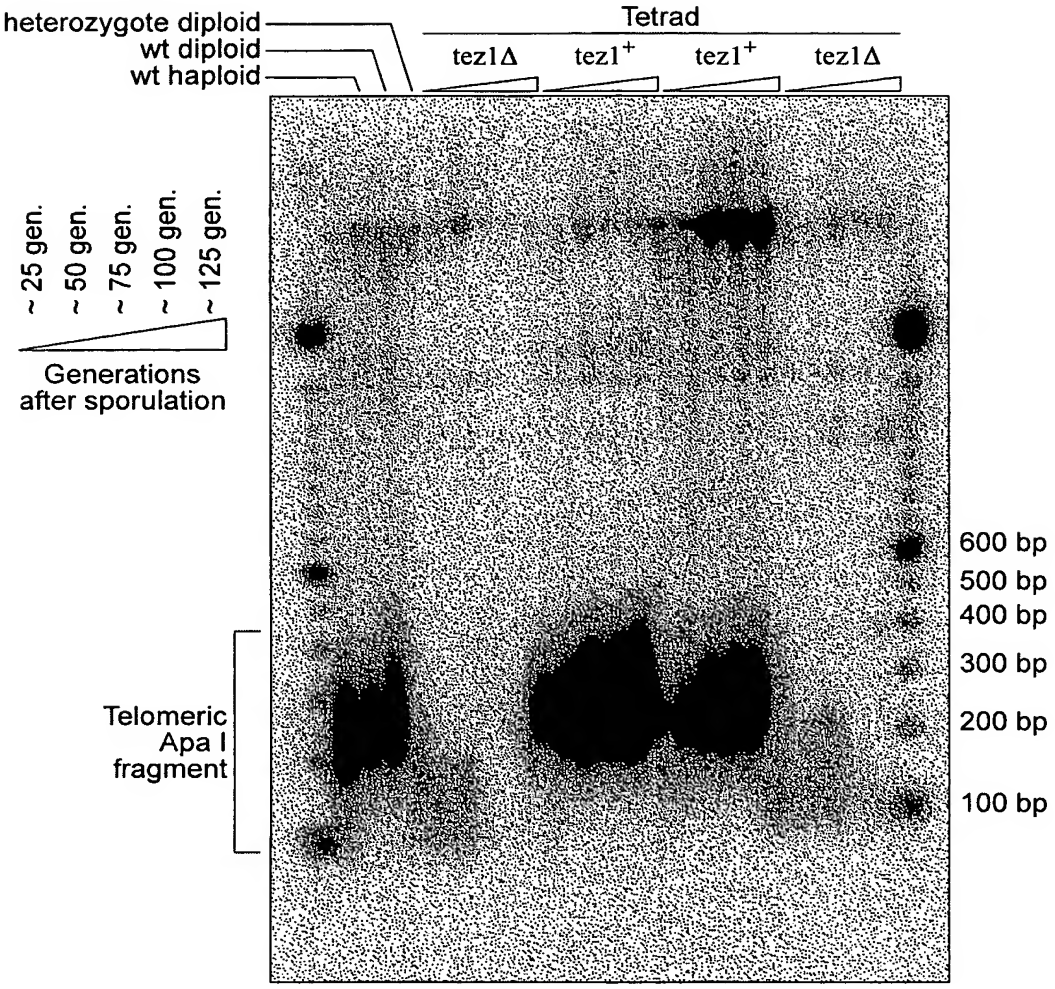

heterozygote diploid
wt diploid
wt haploid
Tetrad
tez1Δ
tez1+
tez1+
tez1Δ
~ 25 gen.
~ 50 gen.
~ 75 gen.
~ 100 gen.
~ 125 gen.
Generations after sporulation
600 bp
500 bp
400 bp
300 bp
200 bp
100 bp
Telomeric Apa I fragment

FIG. 45

```
   1 ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga  80
  81 actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta 160
 161 ccaagtataaggacaaaaagaacaacttccttccccctaaagacttttacttttattaatttacttttcaaatatatttcg 240
 241 ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat 320
 321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc 400
 401 ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag 480
 481 gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttgatgcttgcacacgtctagcatg 560
 561 attgagatattcaaaaatttctatccactacaactcctttaacgcggttttatttttctattttctattctcatgttgtt 640
 641 ccaaatatgtatcatctcgtattaggctttttccgttttactcctggaatcgtacctttttcactattccccctaatga 720
 721 ataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa 800
 801 gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
 881 actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgc   958

 959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA  1018
   1 M   T   E   H   H   T   P   K   S   R   I   L   R   F   L   E   N   Q   Y   V    20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG  1078
  21 Y   L   C   T   L   N   D   Y   V   Q   L   V   L   R   G   S   P   A   S   S    40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT  1138
  41 Y   S   N   I   C   E   R   L   R   S   D   V   Q   T   S   F   S   I   F   L    60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA  1198
  61 H   S   T   V   V   G   F   D   S   K   P   D   E   G   V   Q   F   S   S   P    80

1199 AAA TGC TCA CAG TCA GAG gtatatatatttttgttttgatttttttctattcgggatagctaatatatgggcag 1272
  81 K   C   S   Q   S   E                                                           86

1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA  1332
  87 L   I   A   N   V   V   K   Q   M   F   D   E   S   F   E   R   R   R   N   L   106

1333 CTG ATG AAA GGG TTT TCC ATG gtaaggtattctaattgtgaaatatttacctgcaattactgtttcaaagaga 1405
 107 L   M   K   G   F   S   M                                                       113

1406 ttgtatttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT  1469
 114                     N   H   E   D   F   R   A   M   H   V   N   G   V   Q   N   128
```

FIG. 46A

```
1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA  1529
 129 D   L   V   S   T   F   P   N   Y   L   I   S   I   L   E   S   K   N   W   Q    148

1530 CTT TTG TTA GAA AT gtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatag T ATC GGC 1601
 149 L   L   L   E   I                                                       I   G   155

1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC  1661
 156 S   D   A   M   H   Y   L   L   S   K   G   S   I   F   E   A   L   P   N   D    175

1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG  1721
 176 N   Y   L   Q   I   S   G   I   P   L   F   K   N   N   V   F   E   E   T   V    195

1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA  1781
 196 S   K   K   R   K   R   T   I   E   T   S   I   T   Q   N   K   S   A   R   K    215

1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT  1841
 216 E   V   S   W   N   S   I   S   I   S   R   F   S   I   F   Y   R   S   S   Y    235

1842 AAG AAG TTT AAG CAA G gtaactaatactgttatccttcataactaattttag AT CTA TAT TTT AAC    1907
 236 K   K   F   K   Q   D                                         L   Y   F   N      245

1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG  1967
 246 L   H   S   I   C   D   R   N   T   V   H   M   W   L   Q   W   I   F   P   R    265

1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA  2027
 266 Q   F   G   L   I   N   A   F   Q   V   K   Q   L   H   K   V   I   P   L   V    285

2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA  2087
 286 S   Q   S   T   V   V   P   K   R   L   L   K   V   Y   P   L   I   E   Q   T    305

2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT  2147
 306 A   K   R   L   H   R   I   S   L   S   K   V   Y   N   H   Y   C   P   Y   I    325

2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG  2207
 326 D   T   H   D   D   E   K   I   L   S   Y   S   L   K   P   N   Q   V   F   A    345

2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA  2267
 346 F   L   R   S   I   L   V   R   V   F   P   K   L   I   W   G   N   Q   R   I    365
```

FIG. 46B

```
2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaatttattaccactaacgattttaccag AC CTC GAA ACT 2336
 366 F   E   I   I   L   K   D                                           L   E   T   375

2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG  2396
 376 F   L   K   L   S   R   Y   E   S   F   S   L   H   Y   L   M   S   N   I   K    395

2397 gtaatatgccaaatttttttaccattaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA  2465
 396                                       I   S   E   I   E   W   L   V   L   G    405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG  2525
 406 K   R   S   N   A   K   M   C   L   S   D   F   E   K   R   K   Q   I   F   A    425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT  2585
 426 E   F   I   Y   W   L   Y   N   S   F   I   I   P   I   L   Q   S   F   F   Y    445

2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA  2645
 446 I   T   E   S   S   D   L   R   N   R   T   V   Y   F   R   K   D   I   W   K    465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG  2705
 466 L   L   C   R   P   F   I   T   S   M   K   M   E   A   F   E   K   I   N   E    485

2706 gtattttaaagtatttttgcaaaaagctaatattttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT  2775
 486                                       N   N   V   R   M   D   T   Q   K   T    495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG  2835
 496 T   L   P   P   A   V   I   R   L   L   P   K   K   N   T   F   R   L   I   T    515

2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaatttttggtcatcaatgtactttacttctaatctatta 2906
 516 N   L   R   K   R   F   L   I   K                                               524

2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG  2967
 525         M   G   S   N   K   K   M   L   V   S   T   N   Q   T   L   R   P   V    542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG  3027
 543 A   S   I   L   K   H   L   I   N   E   E   S   S   G   I   P   F   N   L   E    562

3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088
 563 V   Y   M   K   L   L   T   F   K   K   D   L   L   K   H   R   M   F   G        581
```

FIG. 46C

```
3089 tatataatgcgcgattcctcattattaattttgcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA   3155
 582                                       R   K   K   Y   F   V   R   I   D   I     591

3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC  3215
 592 K   S   C   Y   D   R   I   K   Q   D   L   M   F   R   I   V   K   K   K   L    611

3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT  3275
 612 K   D   P   E   F   V   I   R   K   Y   A   T   I   H   A   T   S   D   R   A    631

3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttttcattggaatttttttaacaa 3343
 632 T   K   N   F   V   S   E   A   F   S   Y   F                                    643

3344 attctttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA  3405
 644               D   M   V   P   F   E   K   V   V   Q   L   L   S   M   K   T    659

3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT  3465
 660 S   D   T   L   F   V   D   F   V   D   Y   W   T   K   S   S   S   E   I   F    679

3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca 3532
 680 K   M   L   K   E   H   L   S   G   H   I   V   K                                692

3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA    3593
 693              I   G   N   S   Q   Y   L   Q   K   V   G   I   P   Q   G   S      708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG  3653
 709 I   L   S   S   F   L   C   H   F   Y   M   E   D   L   I   D   E   Y   L   S    728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA  3713
 729 F   T   K   K   K   G   S   V   L   L   R   V   V   D   D   F   L   F   I   T    748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgtcattcc 3777
 749 V   N   K   K   D   A   K   K   F   L   N   L   S   L   R   G                    764

3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA    3840
 765                       F   E   K   H   N   F   S   T   S   L   E   K   T   V      778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA  3900
 779 I   N   F   E   N   S   N   G   I   I   N   N   T   F   F   N   E   S   K   K    798
```

FIG. 46D

```
3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT  3960
 799 R   M   P   F   F   G   F   S   V   N   M   R   S   L   D   T   L   L   A   C    818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG  4020
 819 P   K   I   D   E   A   L   F   N   S   T   S   V   E   L   T   K   H   M   G    838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
 839 K   S   F   F   Y   K   I   L   R                                           S    848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT  4149
 849 S   L   A   S   F   A   Q   V   F   I   D   I   T   H   N   S   K   F   N   S    868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA  4209
 869 C   C   N   I   Y   R   L   G   Y   S   M   C   M   R   A   Q   A   Y   L   K    888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
 889 R   M   K   D   I   F   I   P   Q   R   M   F   I   T   D                       903

4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
 904                         L   L   N   V   I   G   R   K   I   W   K   K   L   A   917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
 918 E   I   L   G   Y   T   S   R   R   F   L   S   S   A   E   V   K   W           935

4402 ggtctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA  4468
 936                                   L   F   C   L   G   M   R   D   G   L   K    946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT  4528
 947 P   S   F   K   Y   H   P   C   F   E   Q   L   I   Y   Q   F   Q   S   L   T    966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA  4588
 967 D   L   I   K   P   L   R   P   V   L   R   Q   V   L   F   L   H   R   R   I    986

4589 GCT GAT TAA tgtcattttcaatttattatatacatcctttattactggtgtcttaaacaatattattactaagtata 4665
 987 A   D   *                                                                       989
```

FIG. 46E

```
4666 gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattgacttgtct 4745
4746 ttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaaca 4825
4826 ttaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttttctataatgaataatgcccgcacta 4905
4906 atgcaaaaagacgaagattatcttctaaacaaggggattaagcatatccgaaggaaaagagagtaatatacccagtgtt 4985
4986 gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc 5065
5066 cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcattta 5145
5146 atgtcttatataaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305
5306 tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgc 5385
5386 aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata 5465
5466 acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc  5544
```

FIG. 46F

```
                                1
                           met ser val tyr val val glu leu leu
GCCAAGTTCCTGCACTGGCTG      ATG AGT GTG TAC GTC GTC GAG CTG CTC

 10                                                  20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

                        30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

 40                                                  50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

                        60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

 70                                                  80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

                        90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

100                                                 110
glu lys     ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

                       120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130                                                 140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

                       150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

160                                                 170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

                       180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

190                                                 200
thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG
```

FIG. 47A

```
                    210
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220                                         230
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

                    240
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250                                         260
arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

                    270
thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280                                         290
arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

                    300
val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310                                         320
phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

                    330
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340                                         350
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

                    360
phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370                                         380
arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

                    390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400                                         410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG
```

FIG. 47B

```
                    420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430                                         440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

                    450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460                                         470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

                    480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490                                         500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

                    510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520                                         530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

                    540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550                                         560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC

CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT

CCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCTTCGCCCTGCCTTCC

TTTGCCTTCCACCCCCACCATTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG

AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG

GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT

TTTCAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAAA
```

FIG. 47C

```
Motif -1
Ep p123          ...LVVSLIRCFFYVTEQQKSYSKT...
Sp Tez1          ...FIIPILQSFFYITESSDLRNRT...
Sc Est2          ...LIPKIIQTFFYCTEISSTVTIV...
Hs TCP1          ...YVVELLRSFFYVTETTFQKNRL...
consensus                     FFY TE

                                                  K
Motif 0                     p hhh  K     hR h     R
Ep p123          ...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
Sp Tez1          ...QKTTLPPAVIRLLPKKN--TFRLITNLRKRFL...
Sc Est2          ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
Hs TCP1          ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
consensus                      R  PK      R I

                               AF
Motif A                   h  hDh  GY  h
Ep p123          ...PKLFFATMDIEKCYDSVNREKLSTFLK...
Sp Tez1          ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Sc Est2          ...PELYFMKFDVKSCYDSIPRMECMRILK...
Hs TCP1          ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
consensus                F   D    YD

Motif B                        hPQG   pS hh
Ep p123          ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
Sp Tez1          ...GNSQYLQKVGIPQGSILSSFLCHFYME...
Sc Est2          ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
Hs TCP1          ...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus                     G  QG   S

                           Y
Motif C                  h  F DD hhh
Ep p123          ...PNVNLLMRLTDDYLLITTQENN...
Sp Tez1          ...KKGSVLLRVVDDFLFITVNKKD...
Sc Est2          ...SQDTLILKLADDFLIISTDQQQ...
Hs TCP1          ...RRDGLLLRLVDDFLLVTPHLTH...
consensus                     DD L

Motif D                    Gh h  cK
Ep p123          ...NVSRENGFKFNMKKL...
Sp Tez1          ...LNLSLRGFEKHNFST...
Sc Est2          ...KKLAMGGFQKYNAKA...
Hs TCP1          ...LRTLVRGVPEYGCVV...
consensus                  G
```

FIG. 48

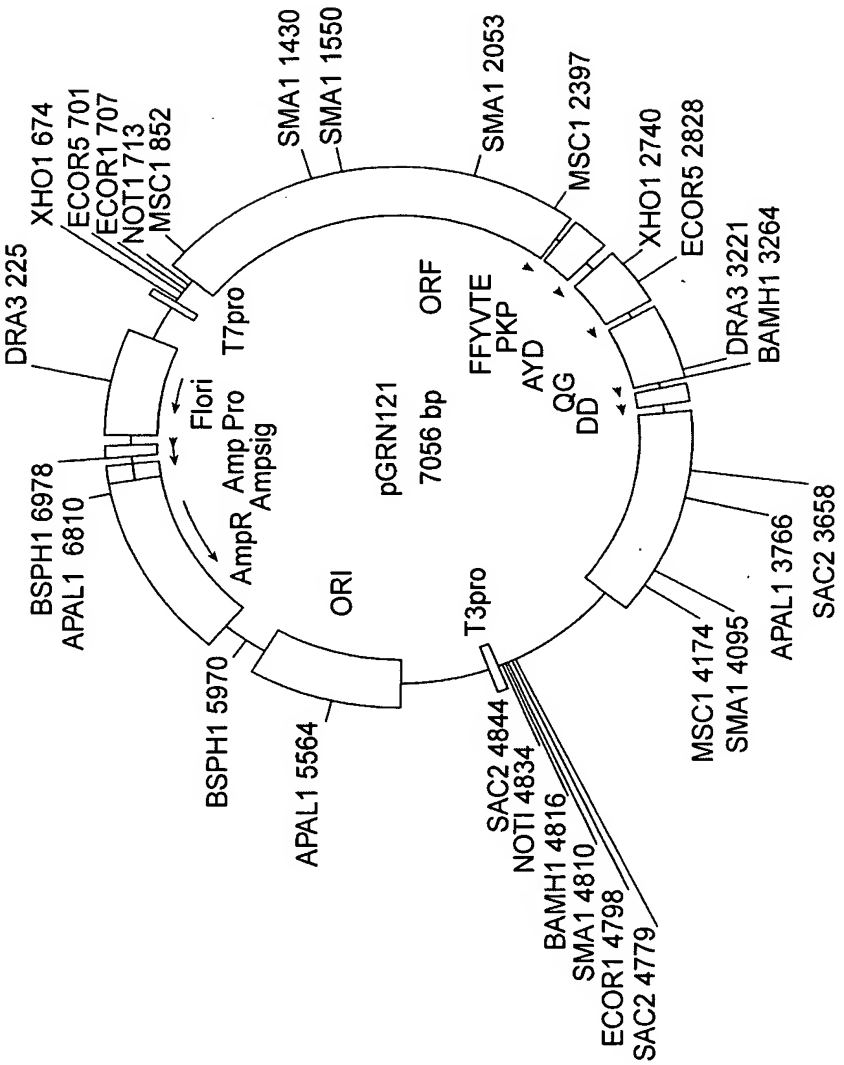

pGRN121
7056 bp
ORF
FFYVTE
PKP
AYD
QG
DD
T7pro
T3pro
ORI
AmpR
Amp Pro
Ampsig
Flori
SMA1 1430
SMA1 1550
SMA1 2053
MSC1 2397
XHO1 2740
ECOR5 2828
DRA3 3221
BAMH1 3264
SAC2 3658
APAL1 3766
SMA1 4095
MSC1 4174
SAC2 4779
ECOR1 4798
SMA1 4810
BAMH1 4816
NOTI 4834
SAC2 4844
APAL1 5564
BSPH1 5970
APAL1 6810
BSPH1 6978
DRA3 225
MSC1 852
NOT1 713
ECOR1 707
ECOR5 701
XHO1 674

FIG. 49

```
   1  GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
  51  CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
 101  AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG
 151  GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG
 201  CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
 251  CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
 301  CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
 351  TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCCC CGAGGCCTTC
 401  ACCACCAGCG TGCGCAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG
 451  GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
 501  TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT GGNTCCCAGC
 551  TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
 601  TCAGGCCCGG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
 651  CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
 701  CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC
 751  GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
 801  CCGTTGGGCA GGGGTCCTGG GCCCACCCGG GCAGGACGCC TGGACCGAGT
 851  GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
 901  CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG
 951  GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
1001  GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCCTCTAC
1051  TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTTCCTACTC AATATATCTG
1101  AGGCCCAGCC TGACTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG
1151  TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA
1201  GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAACCACG
1251  CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
1301  GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
1351  TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG
1401  CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
1451  CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG
1501  AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
1551  GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG
1601  CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
1651  ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
1701  GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
1751  GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
1801  TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
1851  CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
1901  GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG
1951  TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG
2001  GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTCAGCG TGCTCAACTA
2051  CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
2101  ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG
2151  GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
2201  CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA
2251  AACCCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC
2301  GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
2351  AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
2401  GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
2451  GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC
```

FIG. 50A

```
2501  CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG
2551  GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
2601  AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGCGTTTGGT
2651  GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
2701  TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG
2751  CGGAAGACAG TGGTGAACTT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC
2801  GGCTTTTGTT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TGCGGCCTGC
2851  TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC
2901  CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG
2951  GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCACA
3001  GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
3051  ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
3101  GCAGCTCCCA TTTCATCAGC AAGTTTGGAA GAACCCCACA TTTTTCCTGC
3151  GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG
3201  AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC
3251  CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC
3301  GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG
3351  ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC
3401  CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT
3451  GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC
3501  GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCCACAC CCAGGCCCGC
3551  ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
3601  CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA
3651  GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG
3701  CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA
3751  CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC
3801  GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG GAGACCCTGA
3851  GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG
3901  TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT
3951  GGGGGGAGGT GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT
4001  TTGAAAAAAA AAAAAAAAAA AAAAAAAAA
```

FIG. 50B

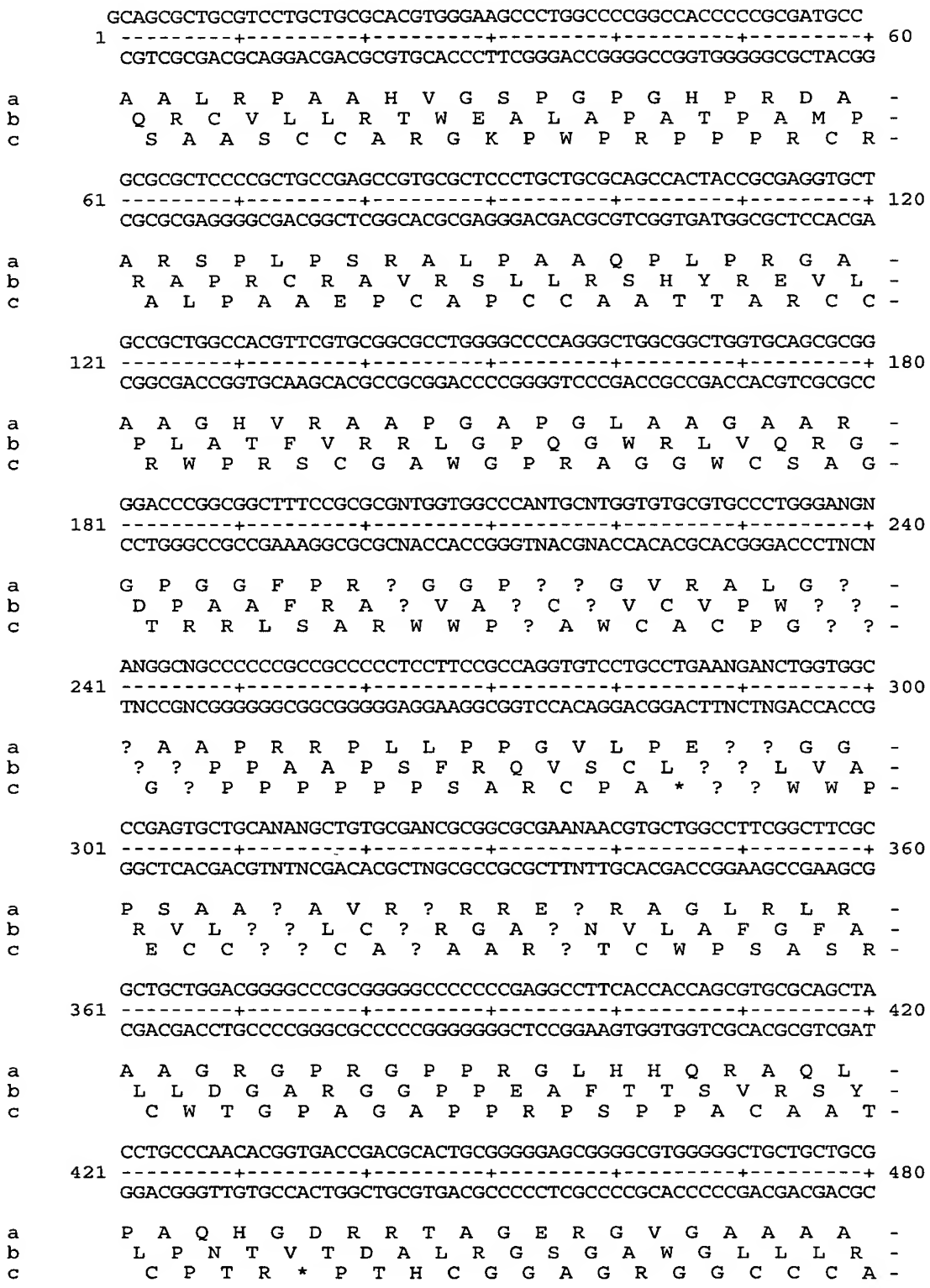

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC
CGTCGCGACGCAGGACGACGCGTGCACCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGG
a A A L R P A A H V G S P G P G H P R D A -
b Q R C V L L R T W E A L A P A T P A M P -
c S A A S C C A R G K P W P R P P P R C R -
GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT
CGCGCGAGGGGCGACGGCTCGGCACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGA
a A R S P L P S R A L P A A Q P L P R G A -
b R A P R C R A V R S L L R S H Y R E V L -
c A L P A A E P C A P C C A A T T A R C C -
GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG
CGGCGACCGGTGCAAGCACGCCGCGGACCCCGGGGTCCCGACCGCCGACCACGTCGCGCC
a A A G H V R A A P G A P G L A A G A A R -
b P L A T F V R R L G P Q G W R L V Q R G -
c R W P R S C G A W G P R A G G W C S A G -
GGACCCGGCGGCTTTCCGCGCGNTGGTGGCCCANTGCNTGGTGTGCGTGCCCTGGGANGN
CCTGGGCCGCCGAAAGGCGCGCNACCACCGGGTNACGNACCACACGCACGGGACCCTNCN
a G P G G F P R ? G G P ? ? G V R A L G ? -
b D P A A F R A ? V A ? C ? V C V P W ? ? -
c T R R L S A R W W P ? A W C A C P G ? ? -
ANGGCNGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAANGANCTGGTGGC
TNCCGNCGGGGGGCGGCGGGGGAGGAAGGCGGTCCACAGGACGGACTTNCTNGACCACCG
a ? A A P R R P L L P P G V L P E ? ? G G -
b ? ? P P A A P S F R Q V S C L ? ? L V A -
c G ? P P P P P P S A R C P A * ? ? W W P -
CCGAGTGCTGCANANGCTGTGCGANCGCGGCGCGAANAACGTGCTGGCCTTCGGCTTCGC
GGCTCACGACGTNTNCGACACGCTNGCGCCGCGCTTNTTGCACGACCGGAAGCCGAAGCG
a P S A A ? A V R ? R R E ? R A G L R L R -
b R V L ? ? L C ? R G A ? N V L A F G F A -
c E C C ? ? C A ? A A R ? T C W P S A S R -
GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA
CGACGACCTGCCCCGGGCGCCCCCGGGGGGGCTCCGGAAGTGGTGGTCGCACGCGTCGAT
a A A G R G P R G P P R G L H H Q R A Q L -
b L L D G A R G G P P E A F T T S V R S Y -
c C W T G P A G A P P R P S P P A C A A T -
CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG
GGACGGGTTGTGCCACTGGCTGCGTGACGCCCCCTCGCCCCGCACCCCCGACGACGACGC
a P A Q H G D R R T A G E R G V G A A A A -
b L P N T V T D A L R G S G A W G L L L R -
c C P T R * P T H C G G A G R G G C C C A -

FIG. 51A

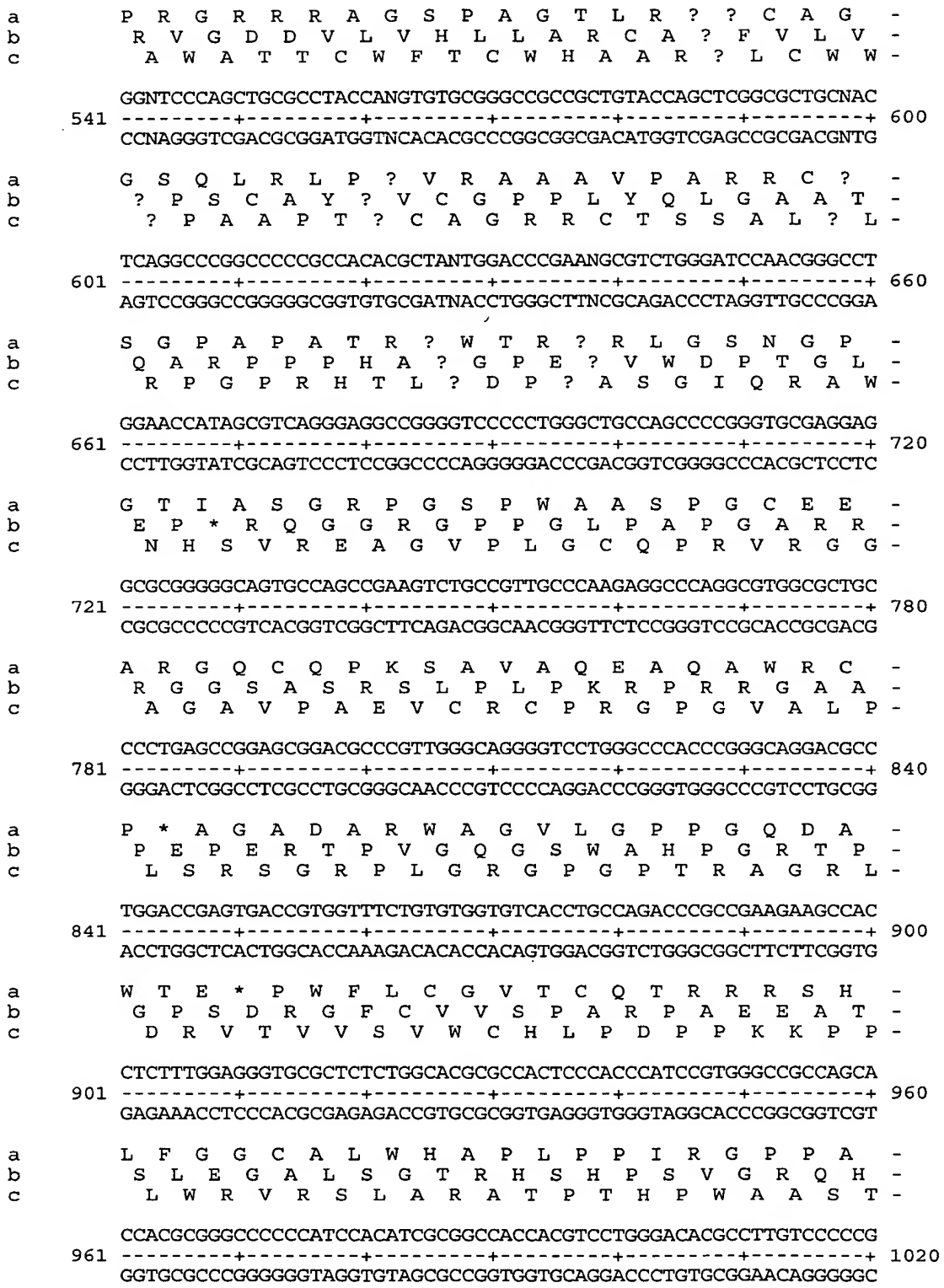

a P R G R R R A G S P A G T L R ? ? C A G -
b R V G D D V L V H L L A R C A ? F V L V -
c A W A T T C W F T C W H A A R ? L C W W -
GGNTCCCAGCTGCGCCTACCANGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCNAC
541 ---------+---------+---------+---------+---------+---------+ 600
CCNAGGGTCGACGCGGATGGTNCACACGCCCGGCGGCGACATGGTCGAGCCGCGACGNTG
a G S Q L R L P ? V R A A A V P A R R C ? -
b ? P S C A Y ? V C G P P L Y Q L G A A T -
c ? P A A P T ? C A G R R C T S S A L ? L -
TCAGGCCCGGCCCCCGCCACACGCTANTGGACCCGAANGCGTCTGGGATCCAACGGGCCT
601 ---------+---------+---------+---------+---------+---------+ 660
AGTCCGGGCCGGGGGCGGTGTGCGATNACCTGGGCTTNCGCAGACCCTAGGTTGCCCGGA
a S G P A P A T R ? W T R ? R L G S N G P -
b Q A R P P P H A ? G P E ? V W D P T G L -
c R P G P R H T L ? D P ? A S G I Q R A W -
GGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAG
661 ---------+---------+---------+---------+---------+---------+ 720
CCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCCGACGGTCGGGGCCCACGCTCCTC
a G T I A S G R P G S P W A A S P G C E E -
b E P * R Q G G R G P P G L P A P G A R R -
c N H S V R E A G V P L G C Q P R V R G G -
GCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGC
721 ---------+---------+---------+---------+---------+---------+ 780
CGCGCCCCCGTCACGGTCGGCTTCAGACGGCAACGGGTTCTCCGGGTCCGCACCGCGACG
a A R G Q C Q P K S A V A Q E A Q A W R C -
b R G G S A S R S L P L P K R P R R G A A -
c A G A V P A E V C R C P R G P G V A L P -
CCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCC
781 ---------+---------+---------+---------+---------+---------+ 840
GGGACTCGGCCTCGCCTGCGGGCAACCCGTCCCCAGGACCCGGGTGGGCCCGTCCTGCGG
a P * A G A D A R W A G V L G P P G Q D A -
b P E P E R T P V G Q G S W A H P G R T P -
c L S R S G R P L G R G P G P T R A G R L -
TGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCAC
841 ---------+---------+---------+---------+---------+---------+ 900
ACCTGGCTCACTGGCACCAAAGACACACCACAGTGGACGGTCTGGGCGGCTTCTTCGGTG
a W T E * P W F L C G V T C Q T R R R S H -
b G P S D R G F C V V S P A R P A E E A T -
c D R V T V V S V W C H L P D P P K K P P -
CTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCA
901 ---------+---------+---------+---------+---------+---------+ 960
GAGAAACCTCCCACGCGAGAGACCGTGCGCGGTGAGGGTGGGTAGGCACCCGGCGGTCGT
a L F G G C A L W H A P L P P I R G P P A -
b S L E G A L S G T R H S H P S V G R Q H -
c L W R V R S L A R A T P T H P W A A S T -
CCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCTGGGACACGCCTTGTCCCCCG
961 ---------+---------+---------+---------+---------+---------+ 1020
GGTGCGCCCGGGGGGTAGGTGTAGCGCCGGTGGTGCAGGACCCTGTGCGGAACAGGGGGC

FIG. 51B

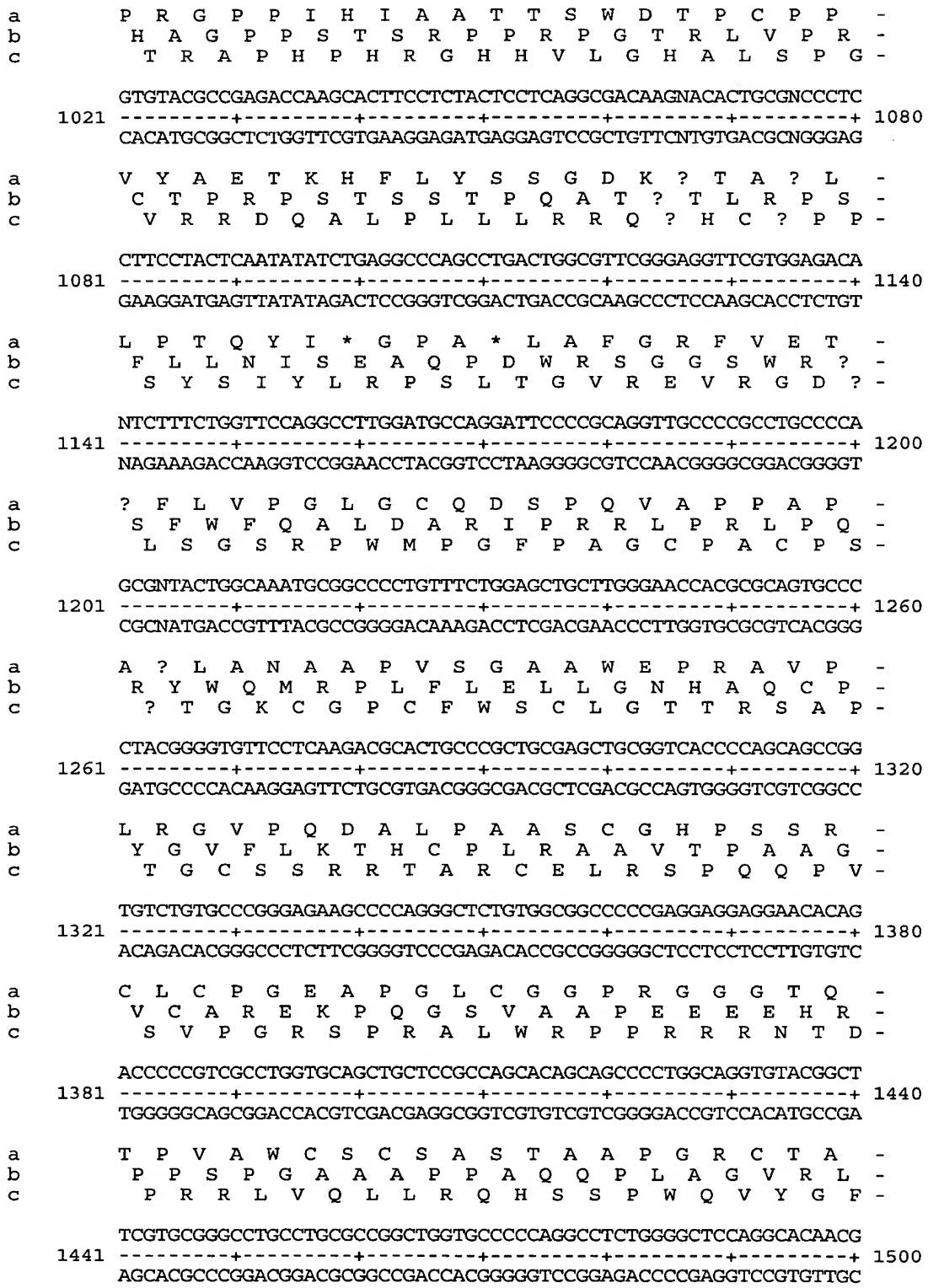

a P R G P P I H I A A T T S W D T P C P P -
b H A G P P S T S R P P R P G T R L V P R -
c T R A P H P H R G H H V L G H A L S P G -
GTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGNACACTGCGNCCCTC
1021 ---------+---------+---------+---------+---------+---------+ 1080
CACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAGTCCGCTGTTCNTGTGACGCNGGGAG
a V Y A E T K H F L Y S S G D K ? T A ? L -
b C T P R P S T S S T P Q A T ? T L R P S -
c V R R D Q A L P L L L R R Q ? H C ? P P -
CTTCCTACTCAATATATCTGAGGCCCAGCCTGACTGGCGTTCGGGAGGTTCGTGGAGACA
1081 ---------+---------+---------+---------+---------+---------+ 1140
GAAGGATGAGTTATATAGACTCCGGGTCGGACTGACCGCAAGCCCTCCAAGCACCTCTGT
a L P T Q Y I * G P A * L A F G R F V E T -
b F L L N I S E A Q P D W R S G G S W R ? -
c S Y S I Y L R P S L T G V R E V R G D ? -
NTCTTTCTGGTTCCAGGCCTTGGATGCCAGGATTCCCCGCAGGTTGCCCCGCCTGCCCCA
1141 ---------+---------+---------+---------+---------+---------+ 1200
NAGAAAGACCAAGGTCCGGAACCTACGGTCCTAAGGGGCGTCCAACGGGGCGGACGGGGT
a ? F L V P G L G C Q D S P Q V A P P A P -
b S F W F Q A L D A R I P R R L P R L P Q -
c L S G S R P W M P G F P A G C P A C P S -
GCGNTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCC
1201 ---------+---------+---------+---------+---------+---------+ 1260
CGCNATGACCGTTTACGCCGGGGACAAAGACCTCGACGAACCCTTGGTGCGCGTCACGGG
a A ? L A N A A P V S G A A W E P R A V P -
b R Y W Q M R P L F L E L L G N H A Q C P -
c ? T G K C G P C F W S C L G T T R S A P -
CTACGGGGTGTTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGG
1261 ---------+---------+---------+---------+---------+---------+ 1320
GATGCCCCACAAGGAGTTCTGCGTGACGGGCGACGCTCGACGCCAGTGGGGTCGTCGGCC
a L R G V P Q D A L P A A S C G H P S S R -
b Y G V F L K T H C P L R A A V T P A A G -
c T G C S S R R T A R C E L R S P Q Q P V -
TGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGAACACAG
1321 ---------+---------+---------+---------+---------+---------+ 1380
ACAGACACGGGCCCTCTTCGGGGTCCCGAGACACCGCCGGGGGCTCCTCCTCCTTGTGTC
a C L C P G E A P G L C G G P R G G G T Q -
b V C A R E K P Q G S V A A P E E E E H R -
c S V P G R S P R A L W R P P R R R N T D -
ACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCT
1381 ---------+---------+---------+---------+---------+---------+ 1440
TGGGGGCAGCGGACCACGTCGACGAGGCGGTCGTGTCGTCGGGGACCGTCCACATGCCGA
a T P V A W C S C S A S T A A P G R C T A -
b P P S P G A A A P P A Q Q P L A G V R L -
c P R R L V Q L L R Q H S S P W Q V Y G F -
TCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACG
1441 ---------+---------+---------+---------+---------+---------+ 1500
AGCACGCCCGGACGGACGCGGCCGACCACGGGGGTCCGGAGACCCCGAGGTCCGTGTTGC

FIG. 51C

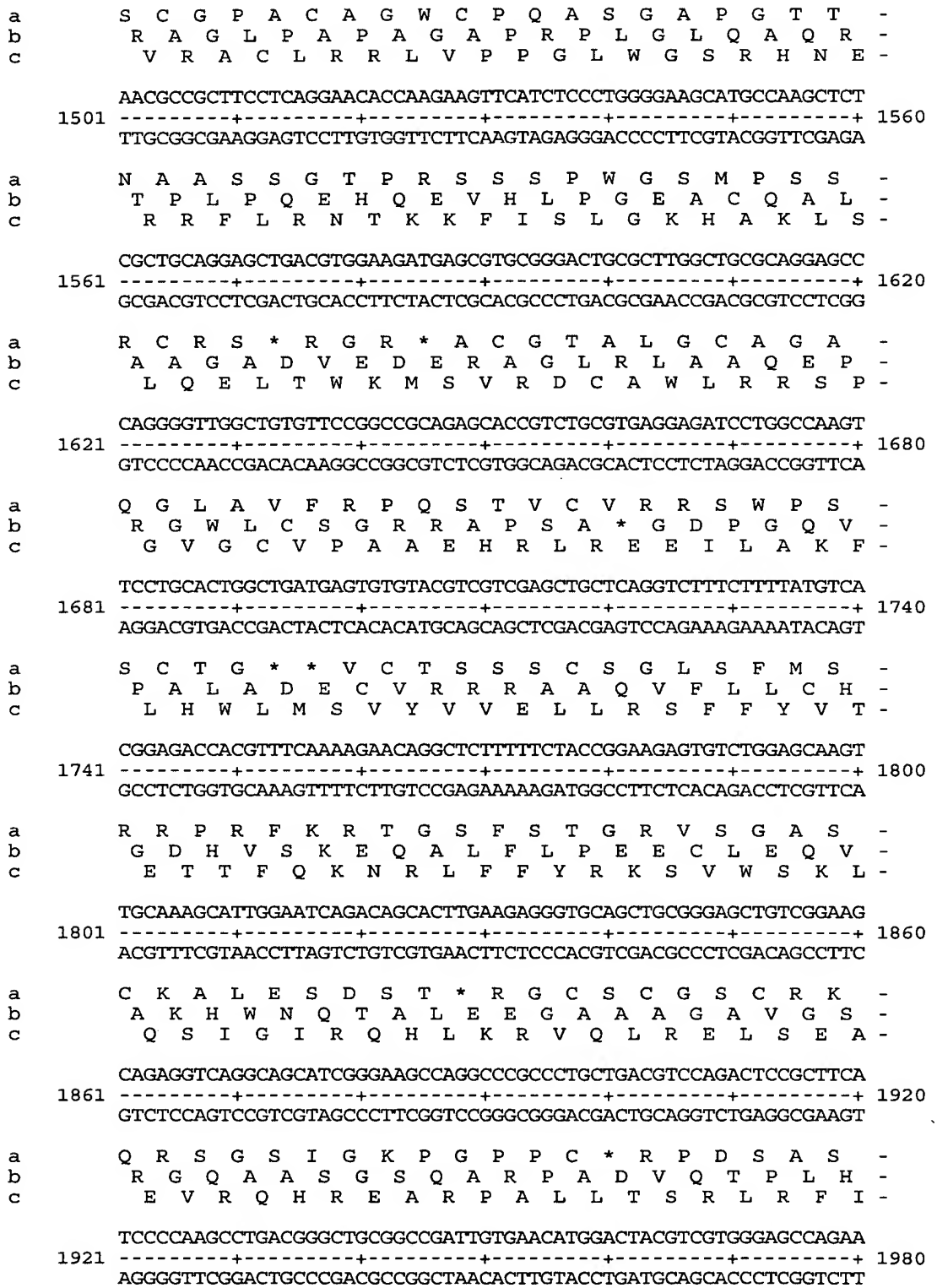

a S C G P A C A G W C P Q A S G A P G T T -
b R A G L P A P A G A P R P L G L Q A Q R -
c V R A C L R R L V P P G L W G S R H N E -
AACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCT
1501 ---------+---------+---------+---------+---------+---------+ 1560
TTGCGGCGAAGGAGTCCTTGTGGTTCTTCAAGTAGAGGGACCCCTTCGTACGGTTCGAGA
a N A A S S G T P R S S S P W G S M P S S -
b T P L P Q E H Q E V H L P G E A C Q A L -
c R R F L R N T K K F I S L G K H A K L S -
CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCC
1561 ---------+---------+---------+---------+---------+---------+ 1620
GCGACGTCCTCGACTGCACCTTCTACTCGCACGCCCTGACGCGAACCGACGCGTCCTCGG
a R C R S * R G R * A C G T A L G C A G A -
b A A G A D V E D E R A G L R L A A Q E P -
c L Q E L T W K M S V R D C A W L R R S P -
CAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGT
1621 ---------+---------+---------+---------+---------+---------+ 1680
GTCCCCAACCGACACAAGGCCGGCGTCTCGTGGCAGACGCACTCCTCTAGGACCGGTTCA
a Q G L A V F R P Q S T V C V R R S W P S -
b R G W L C S G R R A P S A * G D P G Q V -
c G V G C V P A A E H R L R E E I L A K F -
TCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCA
1681 ---------+---------+---------+---------+---------+---------+ 1740
AGGACGTGACCGACTACTCACACATGCAGCAGCTCGACGAGTCCAGAAAGAAAATACAGT
a S C T G * * V C T S S S C S G L S F M S -
b P A L A D E C V R R R A A Q V F L L C H -
c L H W L M S V Y V V E L L R S F F Y V T -
CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGT
1741 ---------+---------+---------+---------+---------+---------+ 1800
GCCTCTGGTGCAAAGTTTTCTTGTCCGAGAAAAAGATGGCCTTCTCACAGACCTCGTTCA
a R R P R F K R T G S F S T G R V S G A S -
b G D H V S K E Q A L F L P E E C L E Q V -
c E T T F Q K N R L F F Y R K S V W S K L -
TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAG
1801 ---------+---------+---------+---------+---------+---------+ 1860
ACGTTTCGTAACCTTAGTCTGTCGTGAACTTCTCCCACGTCGACGCCCTCGACAGCCTTC
a C K A L E S D S T * R G C S C G S C R K -
b A K H W N Q T A L E E G A A A G A V G S -
c Q S I G I R Q H L K R V Q L R E L S E A -
CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCA
1861 ---------+---------+---------+---------+---------+---------+ 1920
GTCTCCAGTCCGTCGTAGCCCTTCGGTCCGGGCGGGACGACTGCAGGTCTGAGGCGAAGT
a Q R S G S I G K P G P P C * R P D S A S -
b R G Q A A S G S Q A R P A D V Q T P L H -
c E V R Q H R E A R P A L L T S R L R F I -
TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAA
1921 ---------+---------+---------+---------+---------+---------+ 1980
AGGGGTTCGGACTGCCCGACGCCGGCTAACACTTGTACCTGATGCAGCACCCTCGGTCTT

FIG. 51D

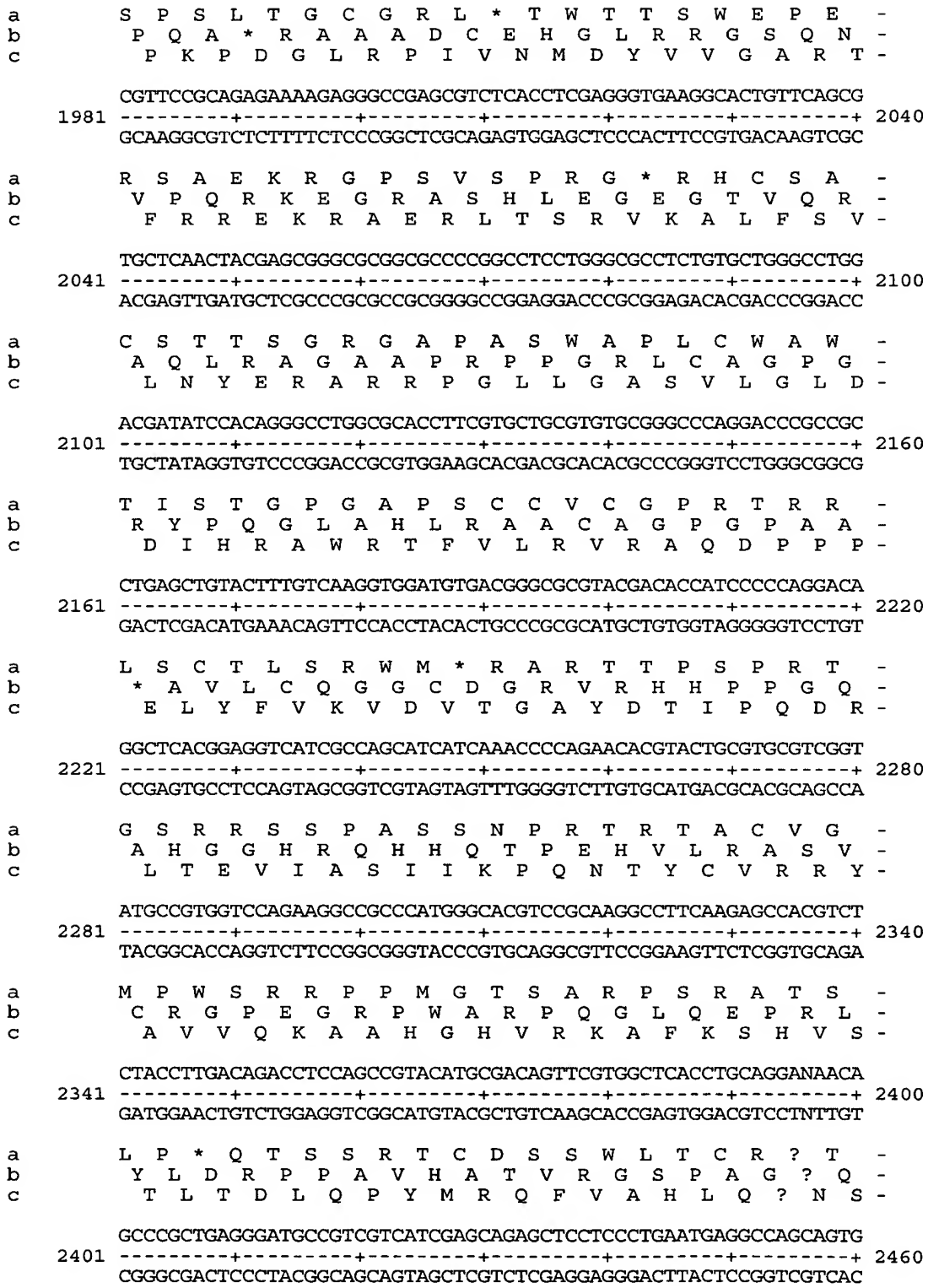

a S P S L T G C G R L * T W T T S W E P E -
b P Q A * R A A A D C E H G L R R G S Q N -
c P K P D G L R P I V N M D Y V V G A R T -
CGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCG
1981 ---------+---------+---------+---------+---------+---------+ 2040
GCAAGGCGTCTCTTTTCTCCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCGC
a R S A E K R G P S V S P R G * R H C S A -
b V P Q R K E G R A S H L E G E G T V Q R -
c F R R E K R A E R L T S R V K A L F S V -
TGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGG
2041 ---------+---------+---------+---------+---------+---------+ 2100
ACGAGTTGATGCTCGCCCGCGCCGCGGGGCCGGAGGACCCGCGGAGACACGACCCGGACC
a C S T T S G R G A P A S W A P L C W A W -
b A Q L R A G A A P R P P G R L C A G P G -
c L N Y E R A R R P G L L G A S V L G L D -
ACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGC
2101 ---------+---------+---------+---------+---------+---------+ 2160
TGCTATAGGTGTCCCGGACCGCGTGGAAGCACGACGCACACGCCCGGGTCCTGGGCGGCG
a T I S T G P G A P S C C V C G P R T R R -
b R Y P Q G L A H L R A A C A G P G P A A -
c D I H R A W R T F V L R V R A Q D P P P -
CTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACA
2161 ---------+---------+---------+---------+---------+---------+ 2220
GACTCGACATGAAACAGTTCCACCTACACTGCCCGCGCATGCTGTGGTAGGGGGTCCTGT
a L S C T L S R W M * R A R T T P S P R T -
b * A V L C Q G G C D G R V R H H P P G Q -
c E L Y F V K V D V T G A Y D T I P Q D R -
GGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGT
2221 ---------+---------+---------+---------+---------+---------+ 2280
CCGAGTGCCTCCAGTAGCGGTCGTAGTAGTTTGGGGTCTTGTGCATGACGCACGCAGCCA
a G S R R S S P A S S N P R T R T A C V G -
b A H G G H R Q H H Q T P E H V L R A S V -
c L T E V I A S I I K P Q N T Y C V R R Y -
ATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCT
2281 ---------+---------+---------+---------+---------+---------+ 2340
TACGGCACCAGGTCTTCCGGCGGGTACCCGTGCAGGCGTTCCGGAAGTTCTCGGTGCAGA
a M P W S R R P P M G T S A R P S R A T S -
b C R G P E G R P W A R P Q G L Q E P R L -
c A V V Q K A A H G H V R K A F K S H V S -
CTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGANAACA
2341 ---------+---------+---------+---------+---------+---------+ 2400
GATGGAACTGTCTGGAGGTCGGCATGTACGCTGTCAAGCACCGAGTGGACGTCCTNTTGT
a L P * Q T S S R T C D S S W L T C R ? T -
b Y L D R P P A V H A T V R G S P A G ? Q -
c T L T D L Q P Y M R Q F V A H L Q ? N S -
GCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTG
2401 ---------+---------+---------+---------+---------+---------+ 2460
CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAGGAGGGACTTACTCCGGTCGTCAC

FIG. 51E

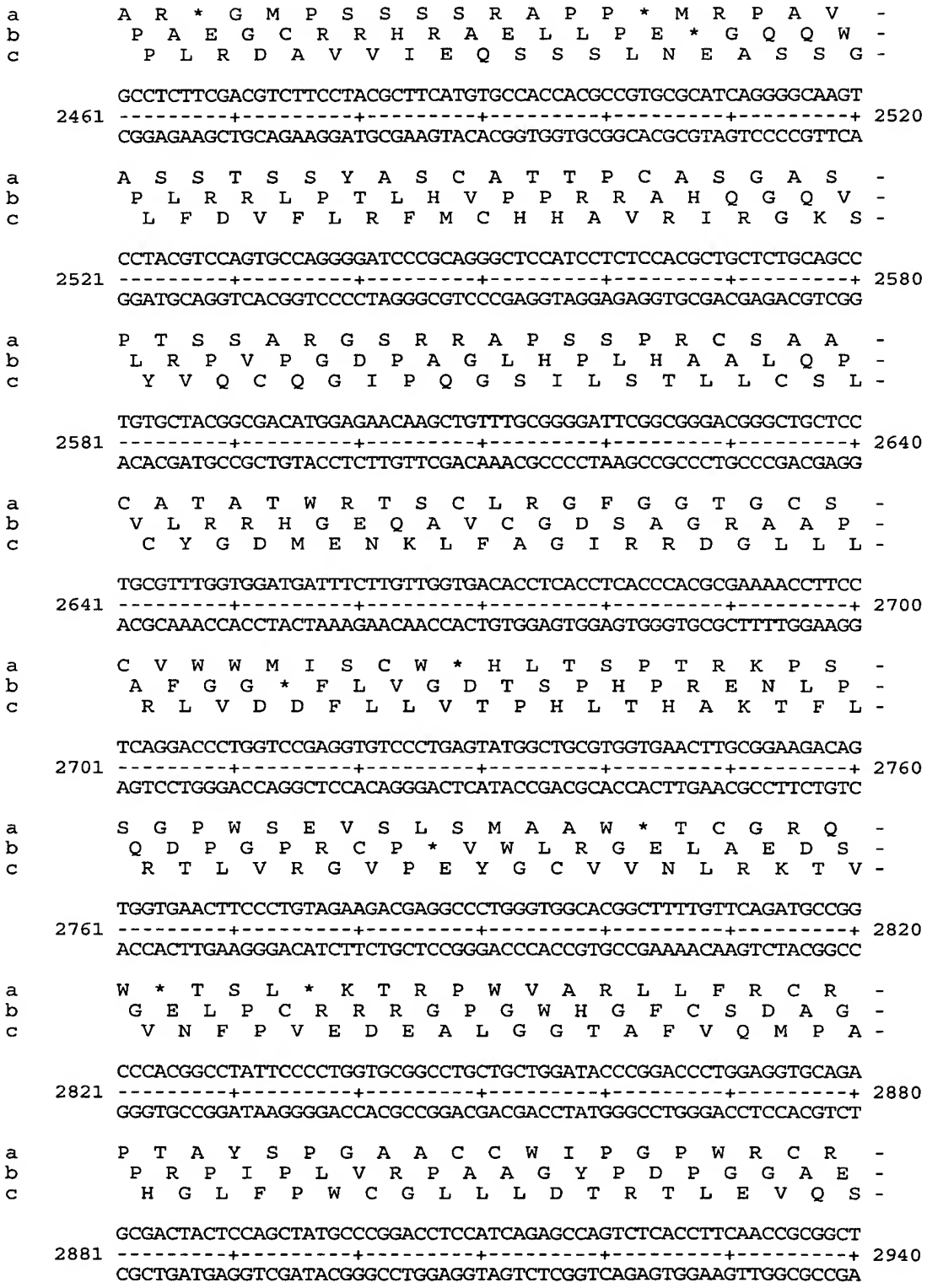

a A R * G M P S S S S R A P P * M R P A V -
b P A E G C R R H R A E L L P E * G Q Q W -
c P L R D A V V I E Q S S S L N E A S S G -
GCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGT
2461 ---------+---------+---------+---------+---------+---------+ 2520
CGGAGAAGCTGCAGAAGGATGCGAAGTACACGGTGGTGCGGCACGCGTAGTCCCCGTTCA
a A S S T S S Y A S C A T T P C A S G A S -
b P L R R L P T L H V P P R R A H Q G Q V -
c L F D V F L R F M C H H A V R I R G K S -
CCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCC
2521 ---------+---------+---------+---------+---------+---------+ 2580
GGATGCAGGTCACGGTCCCCTAGGGCGTCCCGAGGTAGGAGAGGTGCGACGAGACGTCGG
a P T S S A R G S R R A P S S P R C S A A -
b L R P V P G D P A G L H P L H A A L Q P -
c Y V Q C Q G I P Q G S I L S T L L C S L -
TGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCC
2581 ---------+---------+---------+---------+---------+---------+ 2640
ACACGATGCCGCTGTACCTCTTGTTCGACAAACGCCCCTAAGCCGCCCTGCCCGACGAGG
a C A T A T W R T S C L R G F G G T G C S -
b V L R R H G E Q A V C G D S A G R A A P -
c C Y G D M E N K L F A G I R R D G L L L -
TGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCC
2641 ---------+---------+---------+---------+---------+---------+ 2700
ACGCAAACCACCTACTAAAGAACAACCACTGTGGAGTGGAGTGGGTGCGCTTTTGGAAGG
a C V W W M I S C W * H L T S P T R K P S -
b A F G G * F L V G D T S P H P R E N L P -
c R L V D D F L L V T P H L T H A K T F L -
TCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAG
2701 ---------+---------+---------+---------+---------+---------+ 2760
AGTCCTGGGACCAGGCTCCACAGGGACTCATACCGACGCACCACTTGAACGCCTTCTGTC
a S G P W S E V S L S M A A W * T C G R Q -
b Q D P G P R C P * V W L R G E L A E D S -
c R T L V R G V P E Y G C V V N L R K T V -
TGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGG
2761 ---------+---------+---------+---------+---------+---------+ 2820
ACCACTTGAAGGGACATCTTCTGCTCCGGGACCCACCGTGCCGAAAACAAGTCTACGGCC
a W * T S L * K T R P W V A R L L F R C R -
b G E L P C R R R G P G W H G F C S D A G -
c V N F P V E D E A L G G T A F V Q M P A -
CCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGA
2821 ---------+---------+---------+---------+---------+---------+ 2880
GGGTGCCGGATAAGGGGACCACGCCGGACGACGACCTATGGGCCTGGGACCTCCACGTCT
a P T A Y S P G A A C C W I P G P W R C R -
b P R P I P L V R P A A G Y P D P G G A E -
c H G L F P W C G L L L D T R T L E V Q S -
GCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCT
2881 ---------+---------+---------+---------+---------+---------+ 2940
CGCTGATGAGGTCGATACGGGCCTGGAGGTAGTCTCGGTCAGAGTGGAAGTTGGCGCCGA

FIG. 51F

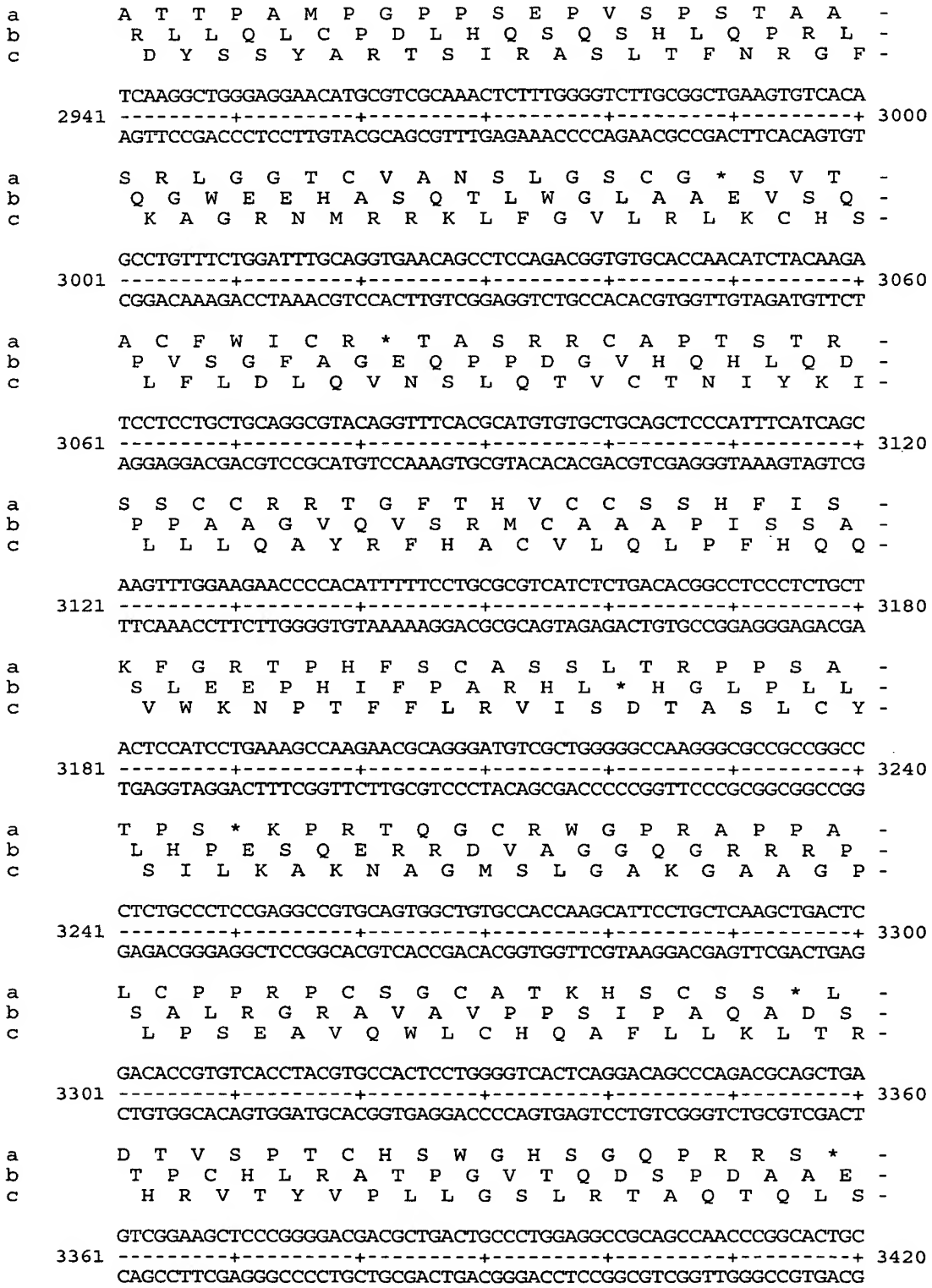

a A T T P A M P G P P S E P V S P S T A A -
b R L L Q L C P D L H Q S Q S H L Q P R L -
c D Y S S Y A R T S I R A S L T F N R G F -
TCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA
2941 ---------+---------+---------+---------+---------+---------+ 3000
AGTTCCGACCCTCCTTGTACGCAGCGTTTGAGAAACCCCAGAACGCCGACTTCACAGTGT
a S R L G G T C V A N S L G S C G * S V T -
b Q G W E E H A S Q T L W G L A A E V S Q -
c K A G R N M R R K L F G V L R L K C H S -
GCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGA
3001 ---------+---------+---------+---------+---------+---------+ 3060
CGGACAAAGACCTAAACGTCCACTTGTCGGAGGTCTGCCACACGTGGTTGTAGATGTTCT
a A C F W I C R * T A S R R C A P T S T R -
b P V S G F A G E Q P P D G V H Q H L Q D -
c L F L D L Q V N S L Q T V C T N I Y K I -
TCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGC
3061 ---------+---------+---------+---------+---------+---------+ 3120
AGGAGGACGACGTCCGCATGTCCAAAGTGCGTACACACGACGTCGAGGGTAAAGTAGTCG
a S S C C R R T G F T H V C C S S H F I S -
b P P A A G V Q V S R M C A A A P I S S A -
c L L L Q A Y R F H A C V L Q L P F H Q Q -
AAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT
3121 ---------+---------+---------+---------+---------+---------+ 3180
TTCAAACCTTCTTGGGGTGTAAAAAGGACGCGCAGTAGAGACTGTGCCGGAGGGAGACGA
a K F G R T P H F S C A S S L T R P P S A -
b S L E E P H I F P A R H L * H G L P L L -
c V W K N P T F F L R V I S D T A S L C Y -
ACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCC
3181 ---------+---------+---------+---------+---------+---------+ 3240
TGAGGTAGGACTTTCGGTTCTTGCGTCCCTACAGCGACCCCCGGTTCCCGCGGCGGCCGG
a T P S * K P R T Q G C R W G P R A P P A -
b L H P E S Q E R R D V A G G Q G R R R P -
c S I L K A K N A G M S L G A K G A A G P -
CTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC
3241 ---------+---------+---------+---------+---------+---------+ 3300
GAGACGGGAGGCTCCGGCACGTCACCGACACGGTGGTTCGTAAGGACGAGTTCGACTGAG
a L C P P R P C S G C A T K H S C S S * L -
b S A L R G R A V A V P P S I P A Q A D S -
c L P S E A V Q W L C H Q A F L L K L T R -
GACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGA
3301 ---------+---------+---------+---------+---------+---------+ 3360
CTGTGGCACAGTGGATGCACGGTGAGGACCCCAGTGAGTCCTGTCGGGTCTGCGTCGACT
a D T V S P T C H S W G H S G Q P R R S * -
b T P C H L R A T P G V T Q D S P D A A E -
c H R V T Y V P L L G S L R T A Q T Q L S -
GTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGC
3361 ---------+---------+---------+---------+---------+---------+ 3420
CAGCCTTCGAGGGCCCCTGCTGCGACTGACGGGACCTCCGGCGTCGGTTGGGCCGTGACG

FIG. 51G

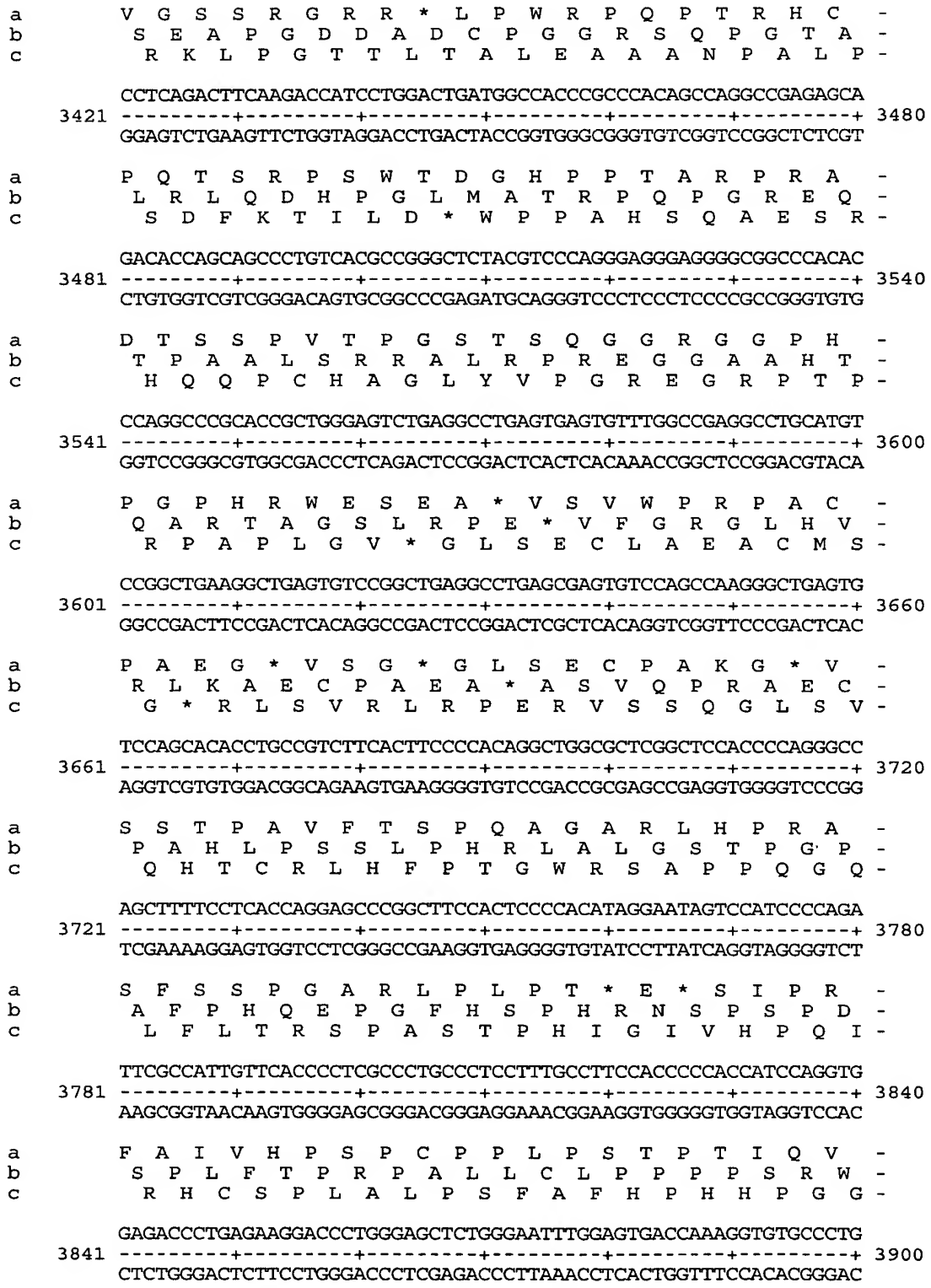

a V G S S R G R R * L P W R P Q P T R H C -
b S E A P G D D A D C P G G R S Q P G T A -
c R K L P G T T L T A L E A A A N P A L P -
CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCA
3421 ---------+---------+---------+---------+---------+---------+ 3480
GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGGCGGGTGTCGGTCCGGCTCTCGT
a P Q T S R P S W T D G H P P T A R P R A -
b L R L Q D H P G L M A T R P Q P G R E Q -
c S D F K T I L D * W P P A H S Q A E S R -
GACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACAC
3481 ---------+---------+---------+---------+---------+---------+ 3540
CTGTGGTCGTCGGGACAGTGCGGCCCGAGATGCAGGGTCCCTCCCTCCCCGCCGGGTGTG
a D T S S P V T P G S T S Q G G R G G P H -
b T P A A L S R R A L R P R E G G A A H T -
c H Q Q P C H A G L Y V P G R E G R P T P -
CCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGT
3541 ---------+---------+---------+---------+---------+---------+ 3600
GGTCCGGGCGTGGCGACCCTCAGACTCCGGACTCACTCACAAACCGGCTCCGGACGTACA
a P G P H R W E S E A * V S V W P R P A C -
b Q A R T A G S L R P E * V F G R G L H V -
c R P A P L G V * G L S E C L A E A C M S -
CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTG
3601 ---------+---------+---------+---------+---------+---------+ 3660
GGCCGACTTCCGACTCACAGGCCGACTCCGGACTCGCTCACAGGTCGGTTCCCGACTCAC
a P A E G * V S G * G L S E C P A K G * V -
b R L K A E C P A E A * A S V Q P R A E C -
c G * R L S V R L R P E R V S S Q G L S V -
TCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCC
3661 ---------+---------+---------+---------+---------+---------+ 3720
AGGTCGTGTGGACGGCAGAAGTGAAGGGGTGTCCGACCGCGAGCCGAGGTGGGGTCCCGG
a S S T P A V F T S P Q A G A R L H P R A -
b P A H L P S S L P H R L A L G S T P G P -
c Q H T C R L H F P T G W R S A P P Q G Q -
AGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA
3721 ---------+---------+---------+---------+---------+---------+ 3780
TCGAAAAGGAGTGGTCCTCGGGCCGAAGGTGAGGGGTGTATCCTTATCAGGTAGGGGTCT
a S F S S P G A R L P L P T * E * S I P R -
b A F P H Q E P G F H S P H R N S P S P D -
c L F L T R S P A S T P H I G I V H P Q I -
TTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTG
3781 ---------+---------+---------+---------+---------+---------+ 3840
AAGCGGTAACAAGTGGGGAGCGGGACGGGAGGAAACGGAAGGTGGGGGTGGTAGGTCCAC
a F A I V H P S P C P P L P S T P T I Q V -
b S P L F T P R P A L L C L P P P P S R W -
c R H C S P L A L P S F A F H P H H P G G -
GAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTG
3841 ---------+---------+---------+---------+---------+---------+ 3900
CTCTGGGACTCTTCCTGGGACCCTCGAGACCCTTAAACCTCACTGGTTTCCACACGGGAC

FIG. 51H

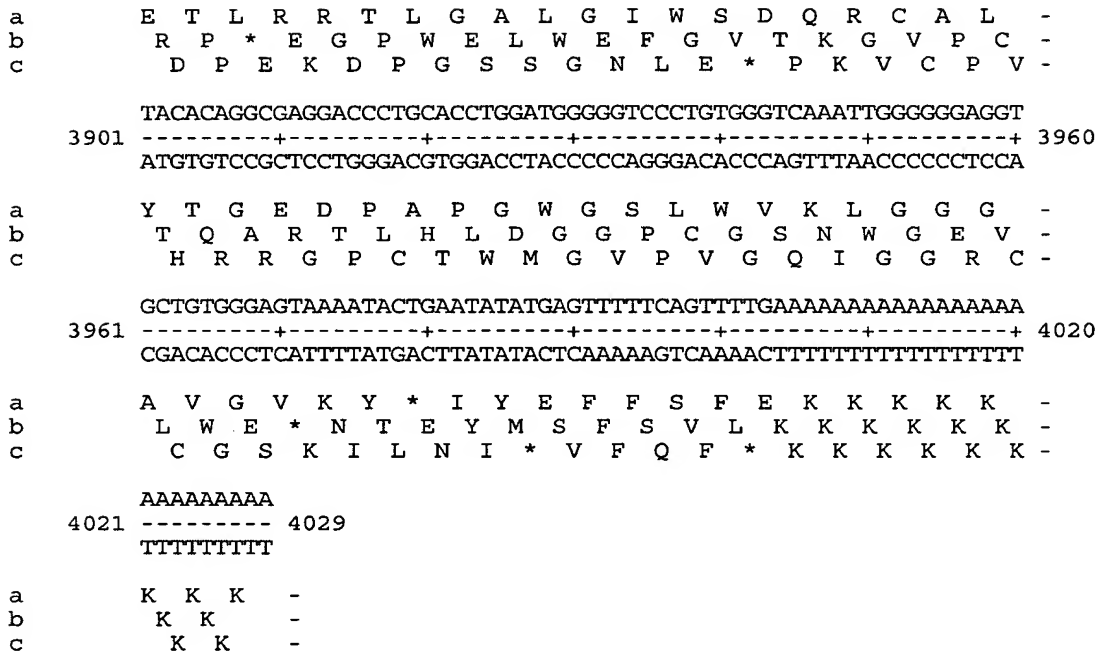

a E T L R R T L G A L G I W S D Q R C A L -
b R P * E G P W E L W E F G V T K G V P C -
c D P E K D P G S S G N L E * P K V C P V -
TACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGT
3901 ---------+---------+---------+---------+---------+---------+ 3960
ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCAGGGACACCCAGTTTAACCCCCCTCCA
a Y T G E D P A P G W G S L W V K L G G G -
b T Q A R T L H L D G G P C G S N W G E V -
c H R R G P C T W M G V P V G Q I G G R C -
GCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAAAAAAAA
3961 ---------+---------+---------+---------+---------+---------+ 4020
CGACACCCTCATTTTATGACTTATATACTCAAAAAGTCAAAACTTTTTTTTTTTTTTTTT
a A V G V K Y * I Y E F F S F E K K K K K -
b L W E * N T E Y M S F S V L K K K K K K -
c C G S K I L N I * V F Q F * K K K K K K -
AAAAAAAAA
4021 --------- 4029
TTTTTTTTT
a K K K -
b K K -
c K K -

FIG. 51I

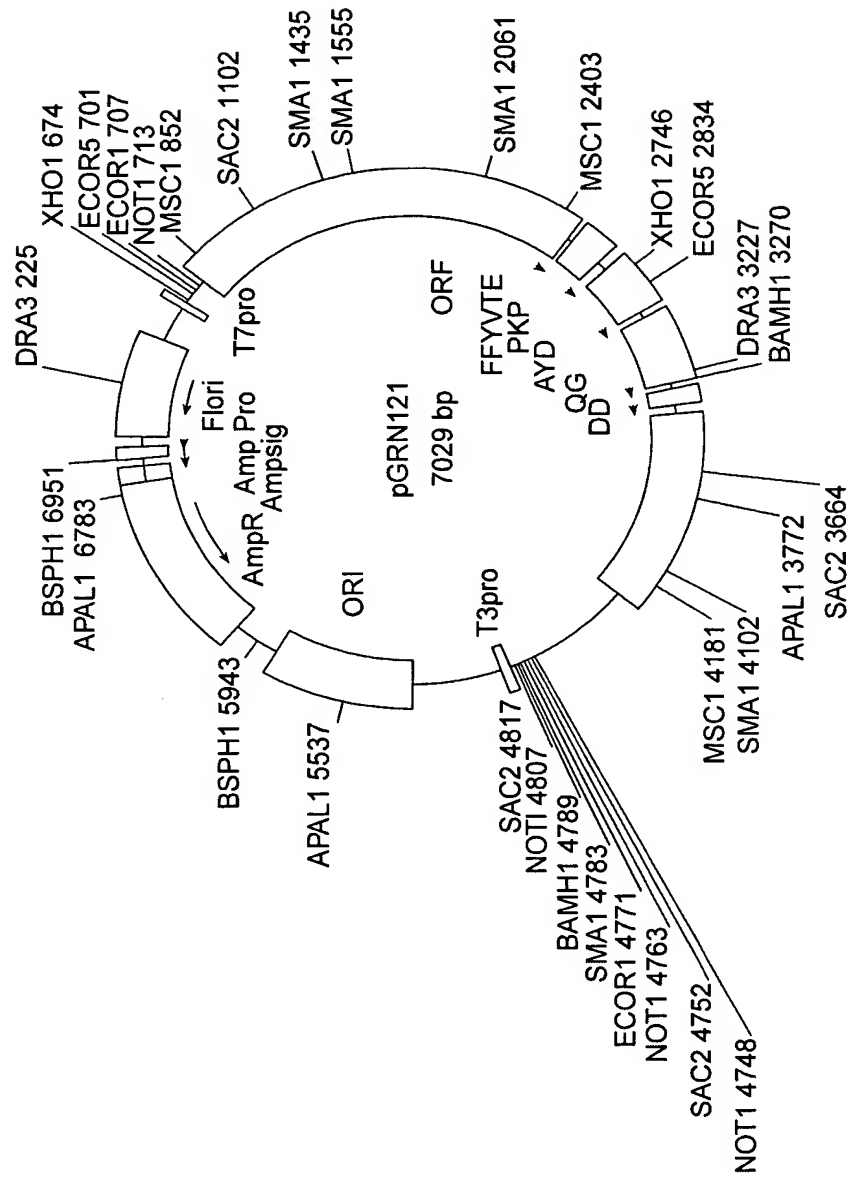

pGRN121
7029 bp
ORF
FFYVTE
PKP
AYD
QG
DD
T7pro
T3pro
Flori
Amp Pro
Ampsig
AmpR
ORI
XHO1 674
ECOR5 701
ECOR1 707
NOT1 713
MSC1 852
SAC2 1102
SMA1 1435
SMA1 1555
SMA1 2061
MSC1 2403
XHO1 2746
ECOR5 2834
DRA3 3227
BAMH1 3270
DRA3 225
BSPH1 6951
APAL1 6783
BSPH1 5943
APAL1 5537
SAC2 4817
NOTI 4807
BAMH1 4789
SMA1 4783
ECOR1 4771
NOT1 4763
SAC2 4752
NOT1 4748
MSC1 4181
SMA1 4102
APAL1 3772
SAC2 3664

FIG. 52

```
                                                                      1
                                                                    met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

                                        10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

             20                                          30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

                                        40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

             50                                          60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

                                        70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

             80                                          90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

                                       100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

            110                                         120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

                                       130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

            140                                         150
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                       160
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

            170                                         180
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                       190
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT
```

FIG. 53A

```
                200                                                 210
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

                                    220
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

                230                                         240
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

                                    250
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

                260                                         270
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

                                    280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG
                290                                         300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

                                    310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

                320                                         330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

                                    340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

                350                                         360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

                                    370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

                380                                         390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

                                    400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

                410                                         420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA
```

FIG. 53B

```
                                        430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

            440                                         450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

                                    460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

            470                                         480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

                                    490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

            500                                         510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

                                    520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

            530                                         540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

                                    550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

            560                                         570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

                                    580
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

            590                                         600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG
                                    610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

            620                                         630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

                                    640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC
```

FIG. 53C

```
                650                                                 660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

                                    670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

            680                                                 690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

                                    700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

            710                                                 720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

                                    730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

            740                                                 750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

                                    760
his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

            770                                                 780
thr asp leu gln pro tyr met arg gln phe val ala his leu gln
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

                                    790
glu thr ser pro leu arg asp ala val val ile glu gln ser ser
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

            800                                                 810
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

                                    820
phe met cys his his ala val arg ile arg gly lys ser tyr val
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

            830                                                 840
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

                                    850
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

            860                                                 870
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG
```

FIG. 53D

```
                                    880
leu val thr pro his leu thr his ala lys thr phe leu arg thr
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

            890                                         900
leu val arg gly val pro glu tyr gly cys val val asn leu arg
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

                                    910
lys thr val val asn phe pro val glu asp glu ala leu gly gly
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

            920                                         930
thr ala phe val gln met pro ala his gly leu phe pro trp cys
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC
                                    940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

            950                                         960
ser ser tyr ala arg thr ser ile arg ala ser leu thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC

                                    970
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

            980                                         990
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

                                    1000
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

            1010                                        1020
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

                                    1030
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

            1040                                        1050
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

                                    1060
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

            1070                                        1080
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

                                    1090
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC
```

FIG. 53E

```
          1100                                                  1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

                                    1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

            1130     1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCC

AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC

GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC

CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG

CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT

CGCCATTGTTCACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA

GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA

CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC

TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGRAAAAAAAAAAAAAAAAAA

AAAAAAAAAA
```

FIG. 53F

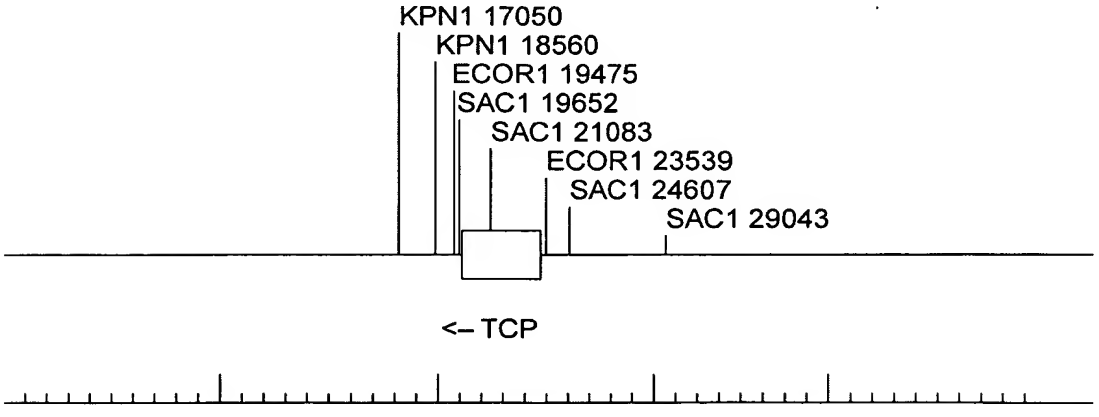


FIG. 54